Structure of everninomicin (Ziracin)

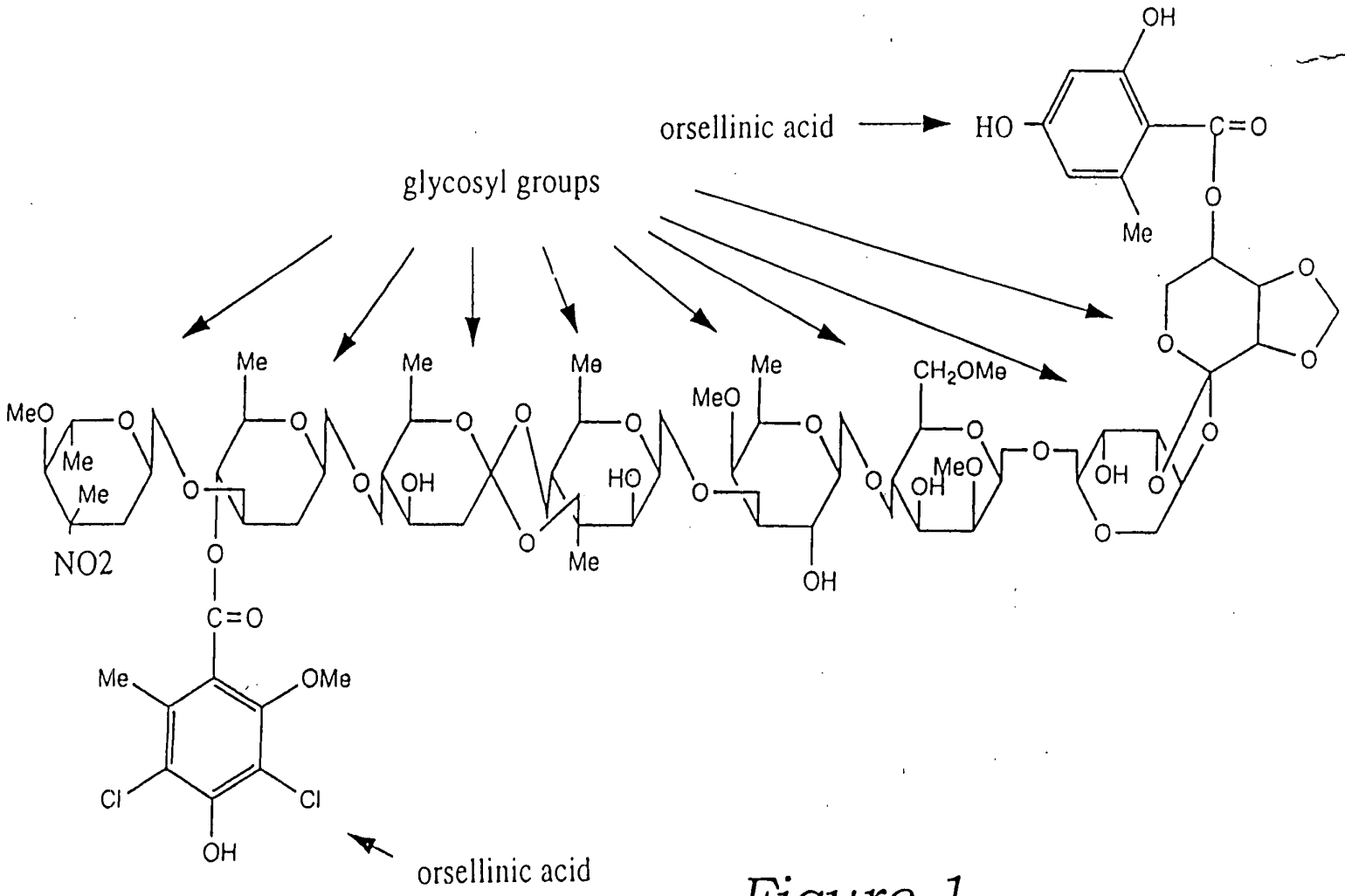


Figure 1

Overlapping cosmids and clones spanning 185 kb of chromosomal DNA containing the Everninomicin Pathway region.

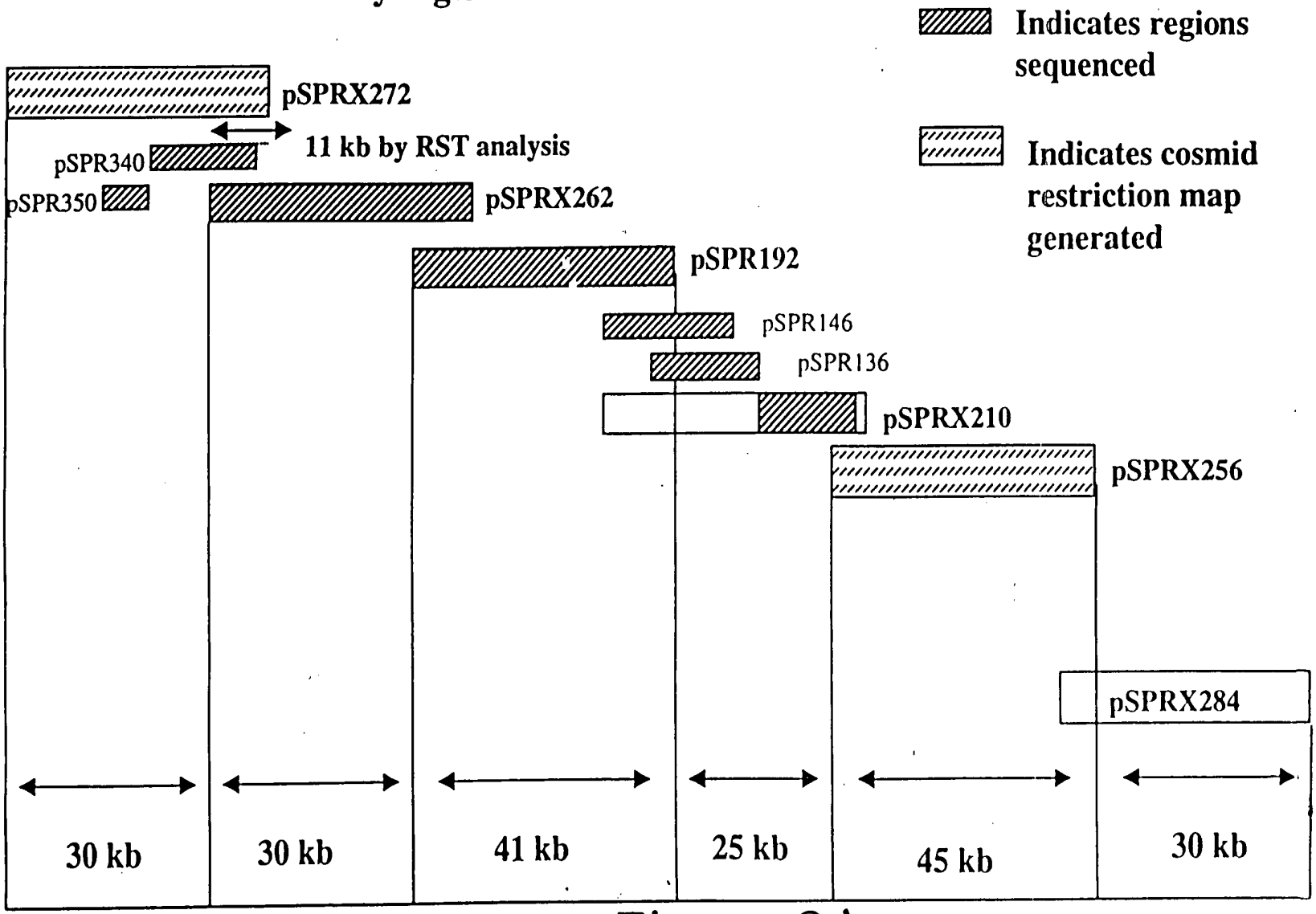


Figure 2A

pSPRX272
37.5kb

Cosmid pSPRX272

Regions sequenced indicated by crosshatches.

Fragments cloned indicated by clone designation benigth fragment.

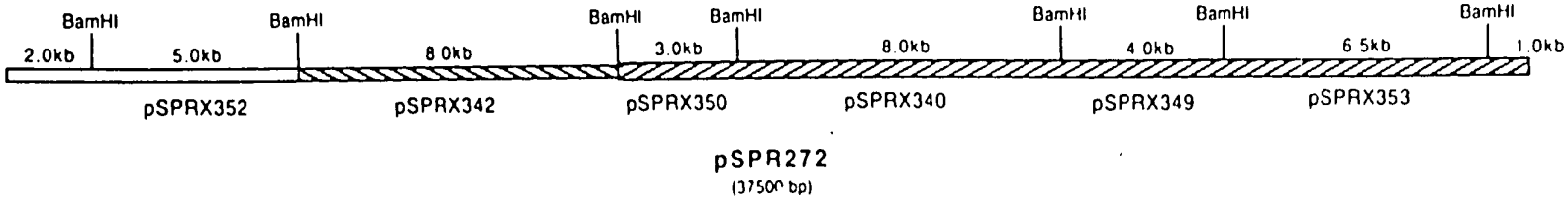


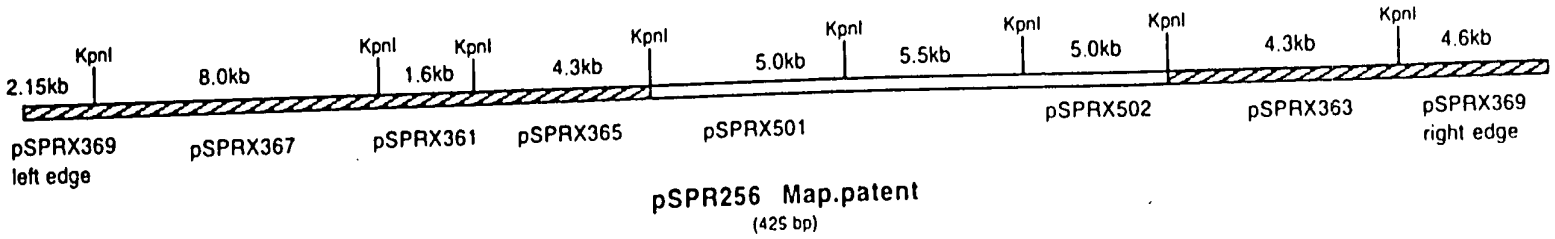
Figure 2B

Cosmid pSPRX256

Regions sequenced indicated by crosshatches.

Fragments cloned indicated by clone designation benigth fragment.

Cosmid
pSPRX256



pSPR256 Map.patent
(425 bp)

Figure 2C

Figure 3 (A)

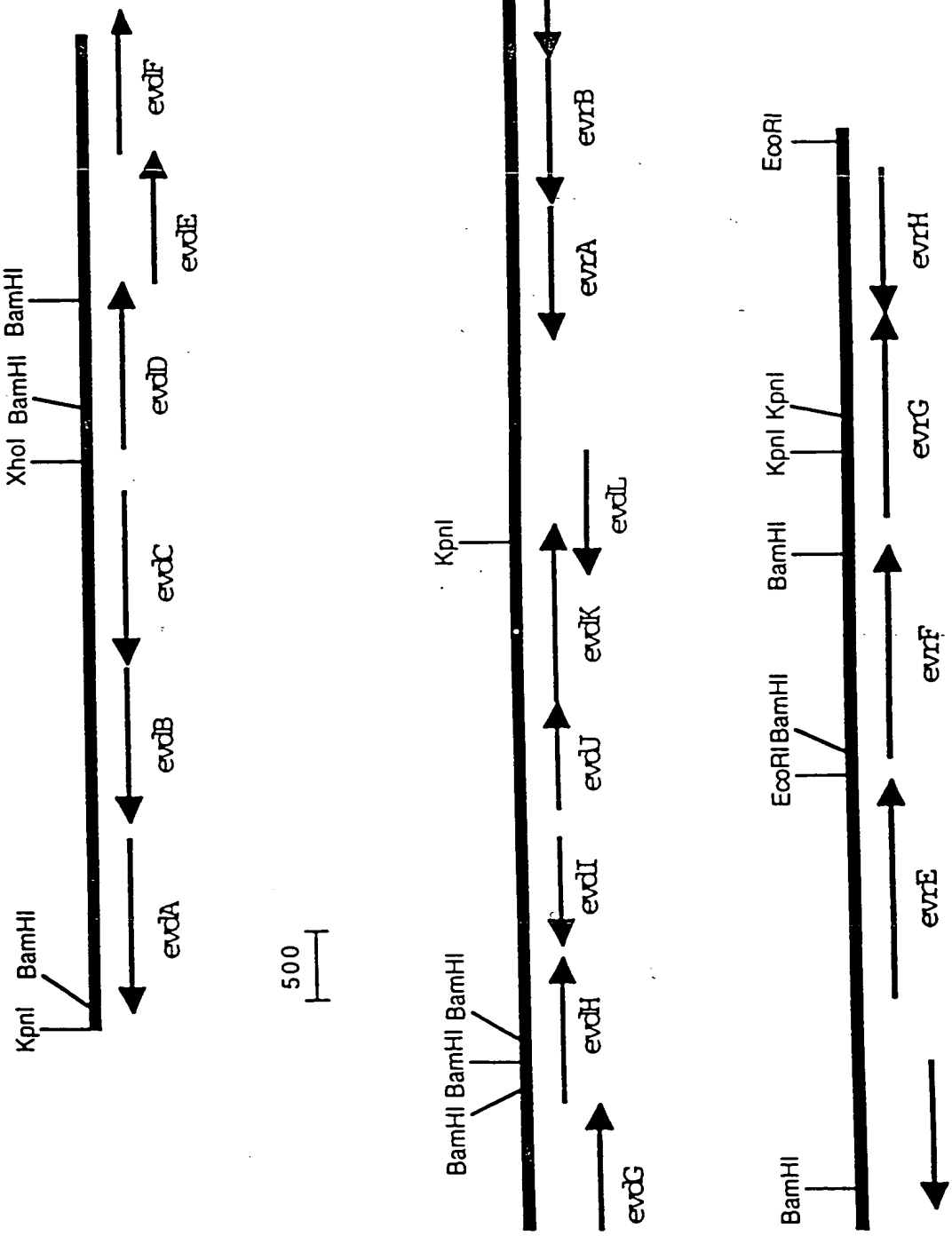

KpnI
BamHI
XhoI
BamHI
BamHI
evdA
evdB
evdC
evdD
evdE
evdF
500
BamHI
BamHI
BamHI
evdG
evdH
evdI
evdJ
evdK
evdL
KpnI
PstI
evrA
evrB
evrC
BamHI
EcoRI
EcoRI
BamHI
KpnI
KpnI
evrD
evrE
evrF
evrG
evrH

Figure 3 (B)

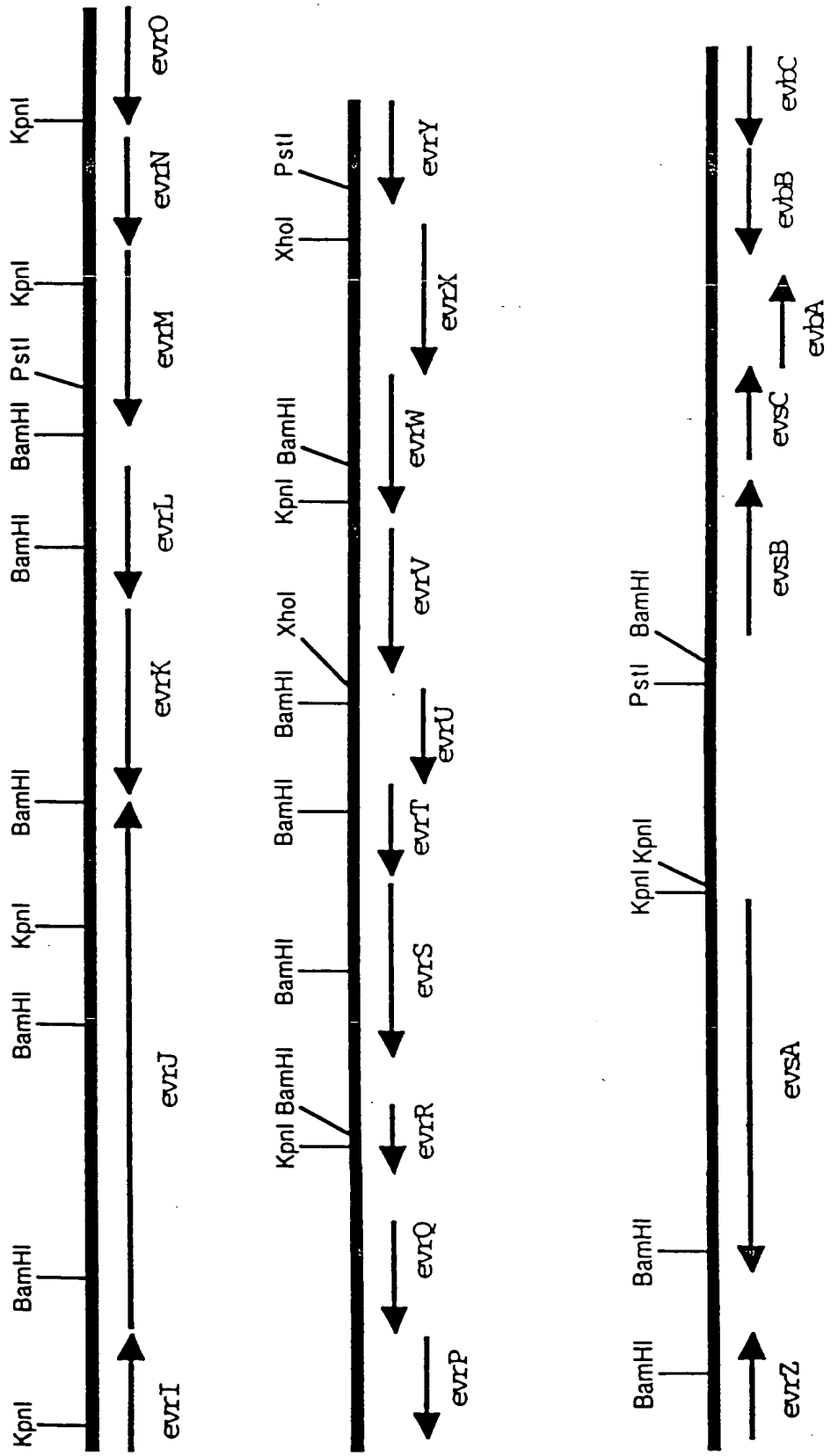

KpnI
BamHI
BamHI
KpnI
BamHI
BamHI
PstI
KpnI
KpnI
evrI
evrJ
evrK
evrL
evrM
evrN
evrO
KpnI BamHI
BamHI
BamHI
BamHI
XhoI
PstI
evrP
evrQ
evrR
evrS
evrT
evrU
evrV
evrW
evrX
evrY
PstI
BamHI
KpnI KpnI
BamHI
BamHI
evrZ
evsA
evsB
evsC
evbA
evbB
evbC

Figure 3 (C)

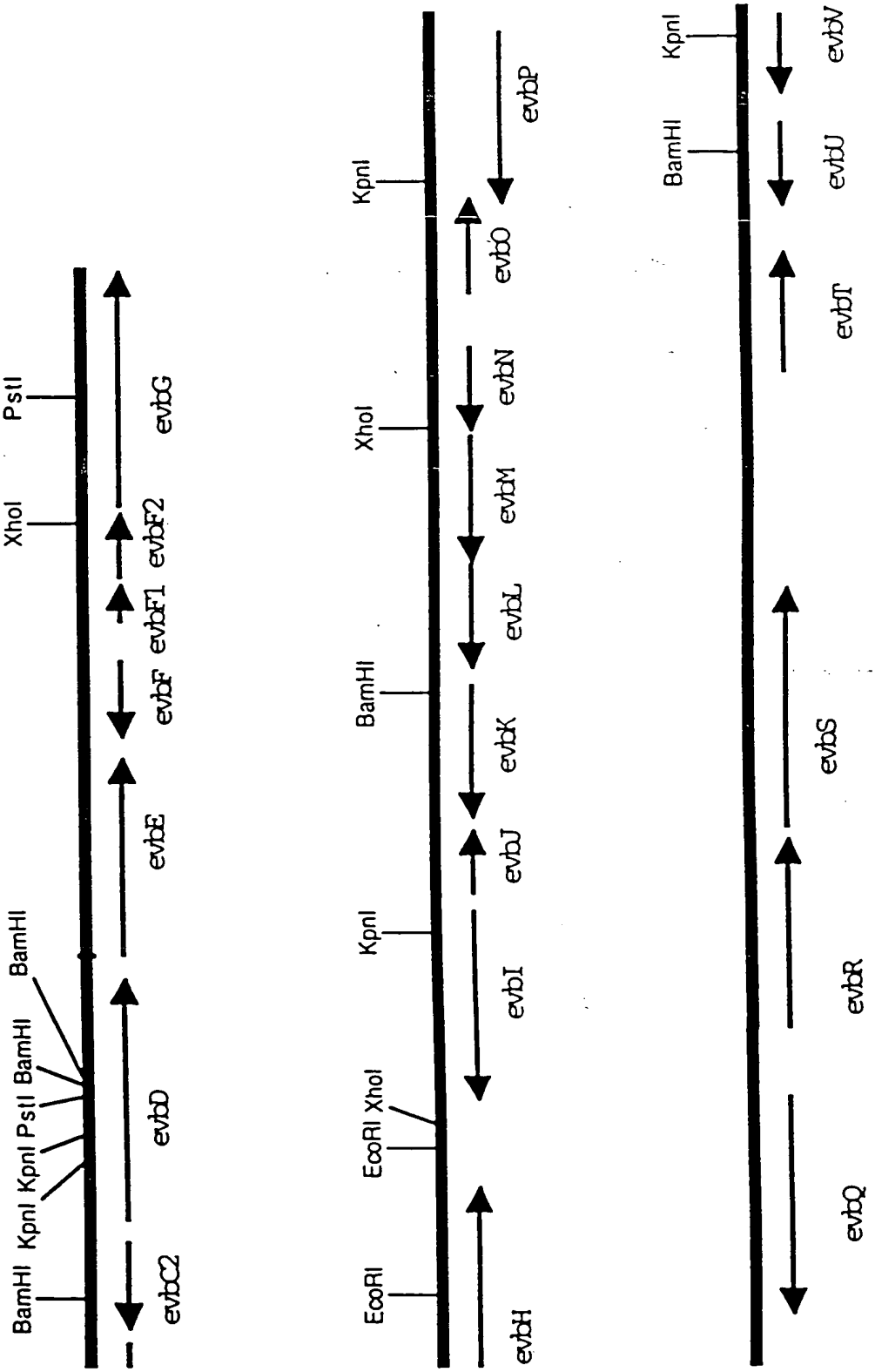

BamHI
KpnI
KpnI
PstI
BamHI
BamHI
PstI
XhoI
evbC2
evbD
evbE
evbF
evbF1
evbF2
evbG
EcoRI
EcoRI
XhoI
KpnI
BamHI
XhoI
KpnI
evbH
evbI
evbJ
evbK
evbL
evbM
evbN
evbO
evbP
BamHI
KpnI
evbQ
evbR
evbS
evbT
evbU
evbV

Figure 3 (D)

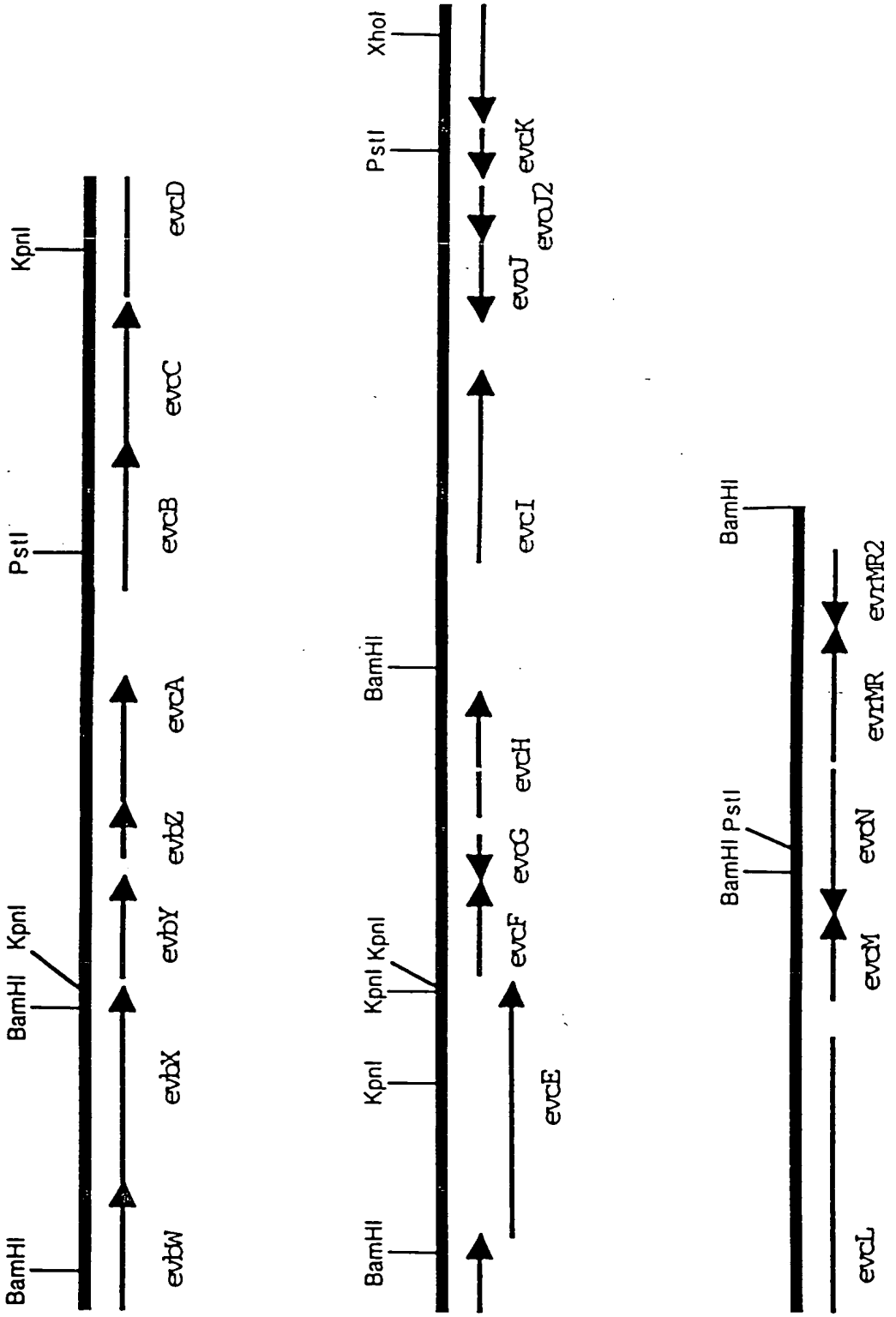

BamHI
evbW
evbX
KpnI
BamHI
evbY
evbZ
PstI
evcA
evcB
KpnI
evcC
evcD
BamHI
KpnI
KpnI
evcE
evcF
evcG
evcH
BamHI
PstI
evcI
evcJ
evcJ2
evcK
XhoI
BamHI
BamHI PstI
evcL
evcM
evcN
evcMR
evcMR2

Figure 4 (A)

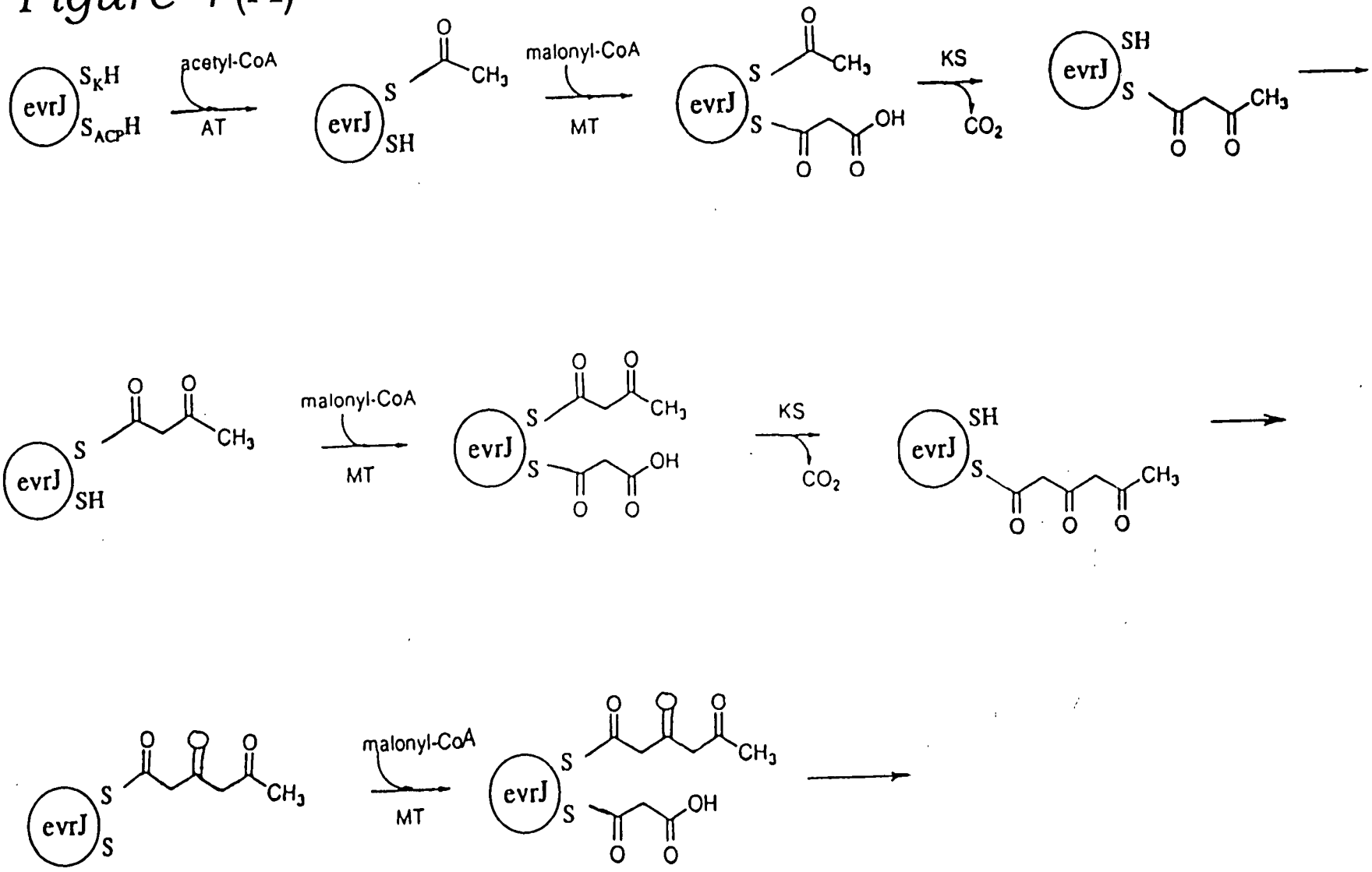


Figure 4 (B)

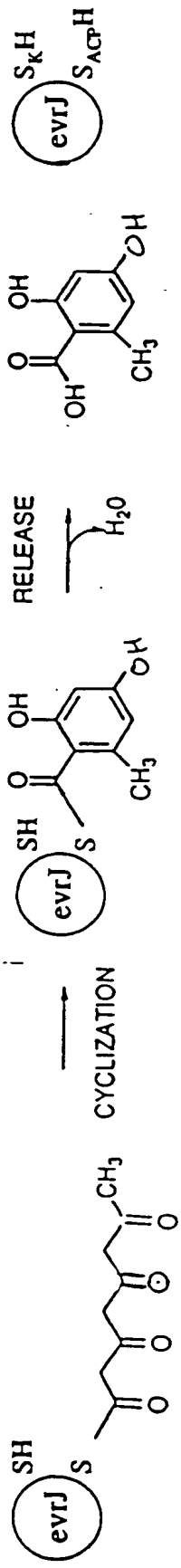
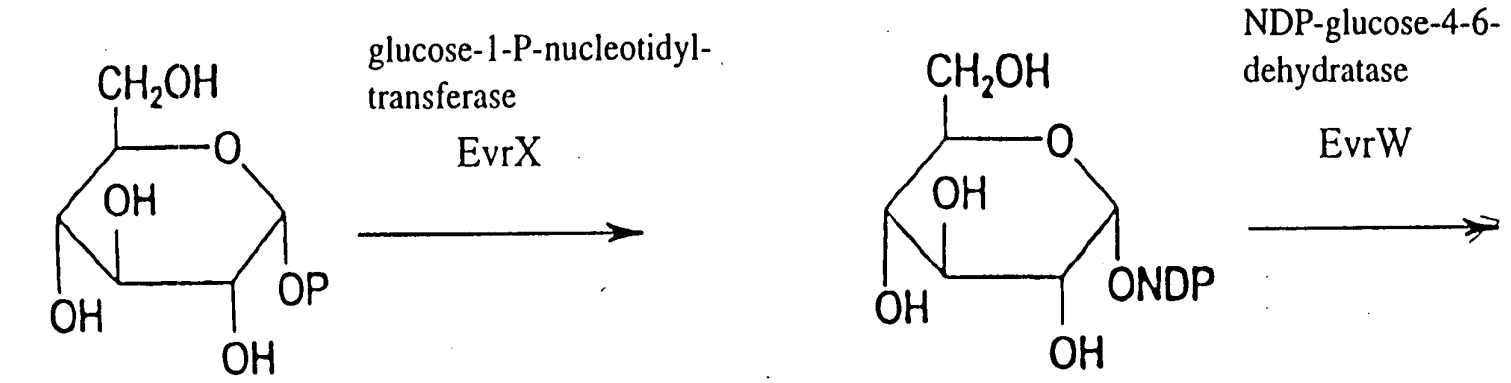

evrJ
SH
S
CH3
O
O
O
O
CYCLIZATION
evrJ
SH
S
O
OH
CH3
OH
RELEASE
H2O
OH
O
OH
CH3
OH
evrJ
SKH
SACPH

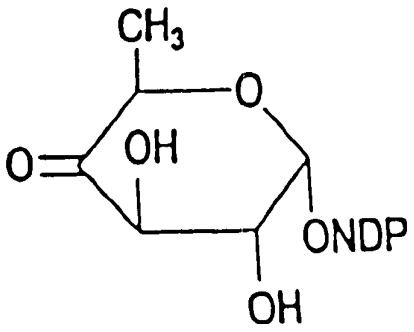
Figure 5 (A)



D-glucose-1-phosphate

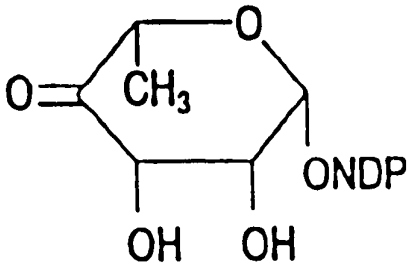
NDP-D-glucose

Figure 5 (B)



NDP-4-keto-6-deoxyglucos
3,5 epimerase

EvrV



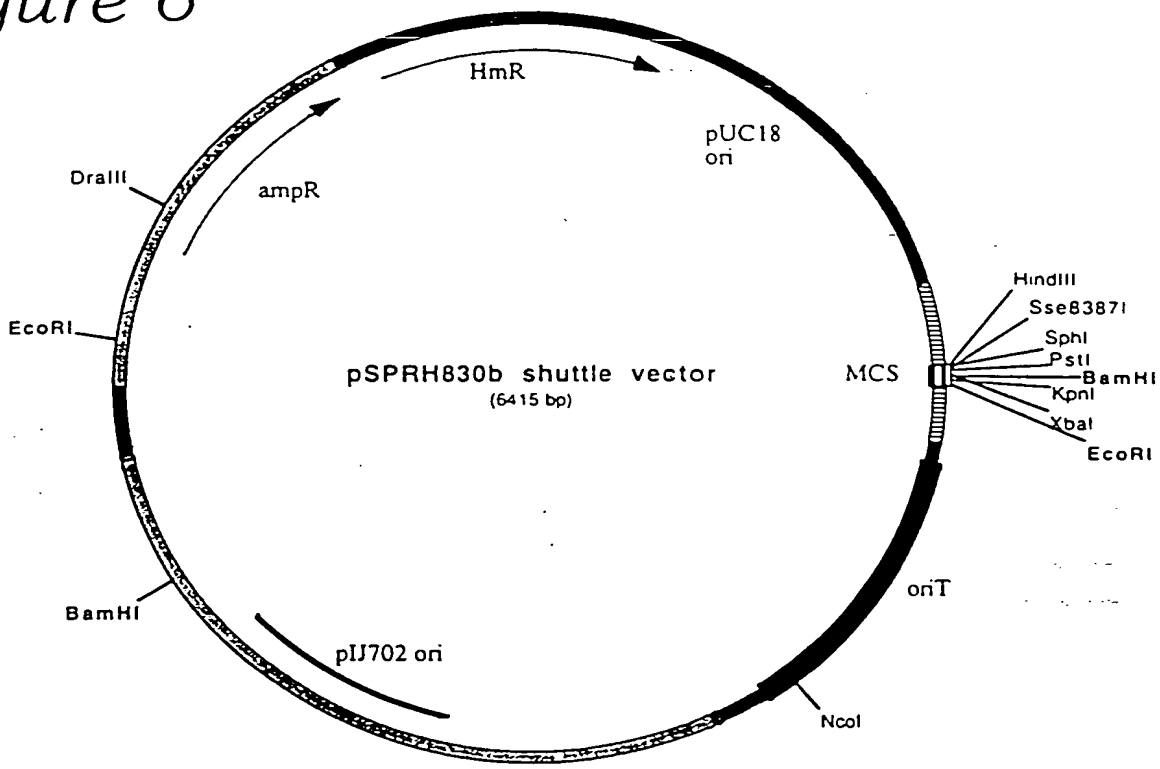
NDP-4-keto-6-deoxy-
D-glucose

NDP-4-keto-rhamnose

Modifications and
Glycosyltransferase
attachment
to Everninomicin

pSPRH830b *E.coli*-Micromonospora shuttle vector

Figure 6

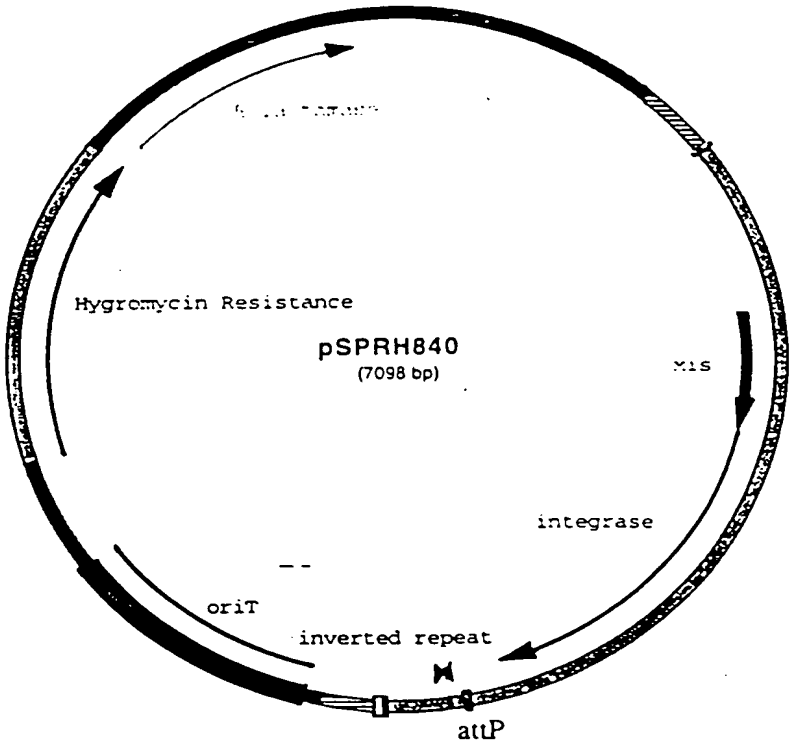


pSPRH830b - pSPRH826b backbone

Function	Source
- Ampicillin resistance	(pUC18)
- Multiple cloning site	(pUC18)
- pUC18 origin	(pUC18)
- Hygromycin resistance	(p16R1)
- oriT (origin of transfer)	(pRL1058)
- pIJ702 origin of replication	(pIJ702)

pSPRH840 integrating vector

Figure 7A



pSPRH840 - pSPRH826b backbone, pMLP1 *xis, int* attP insert

pSPRH840 conjugated from *E. coli* into	HmR transformants obtained
M.carbonacea	+
M.rosaria	-
M.halophitica	+

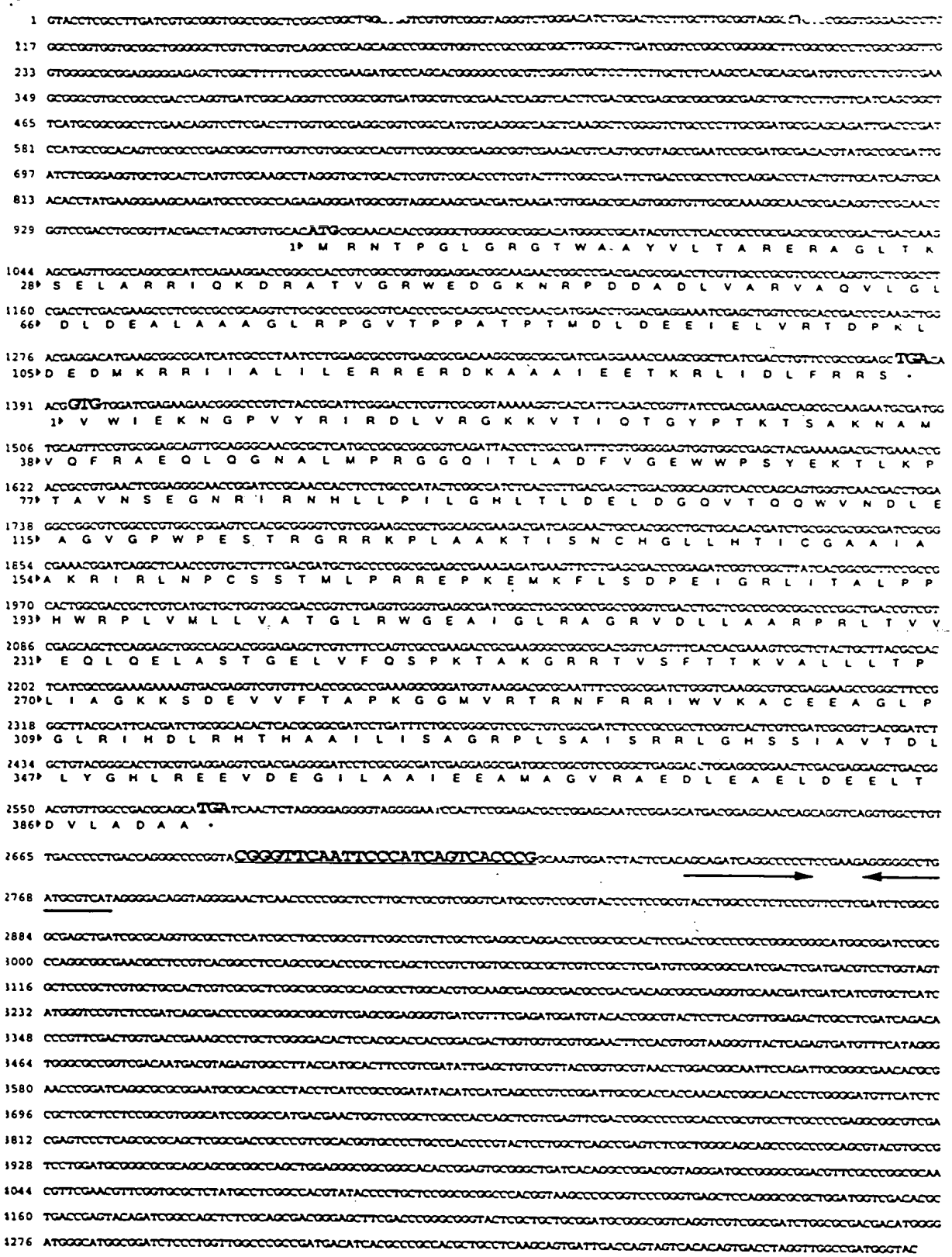


Figure 7B

Figure 8

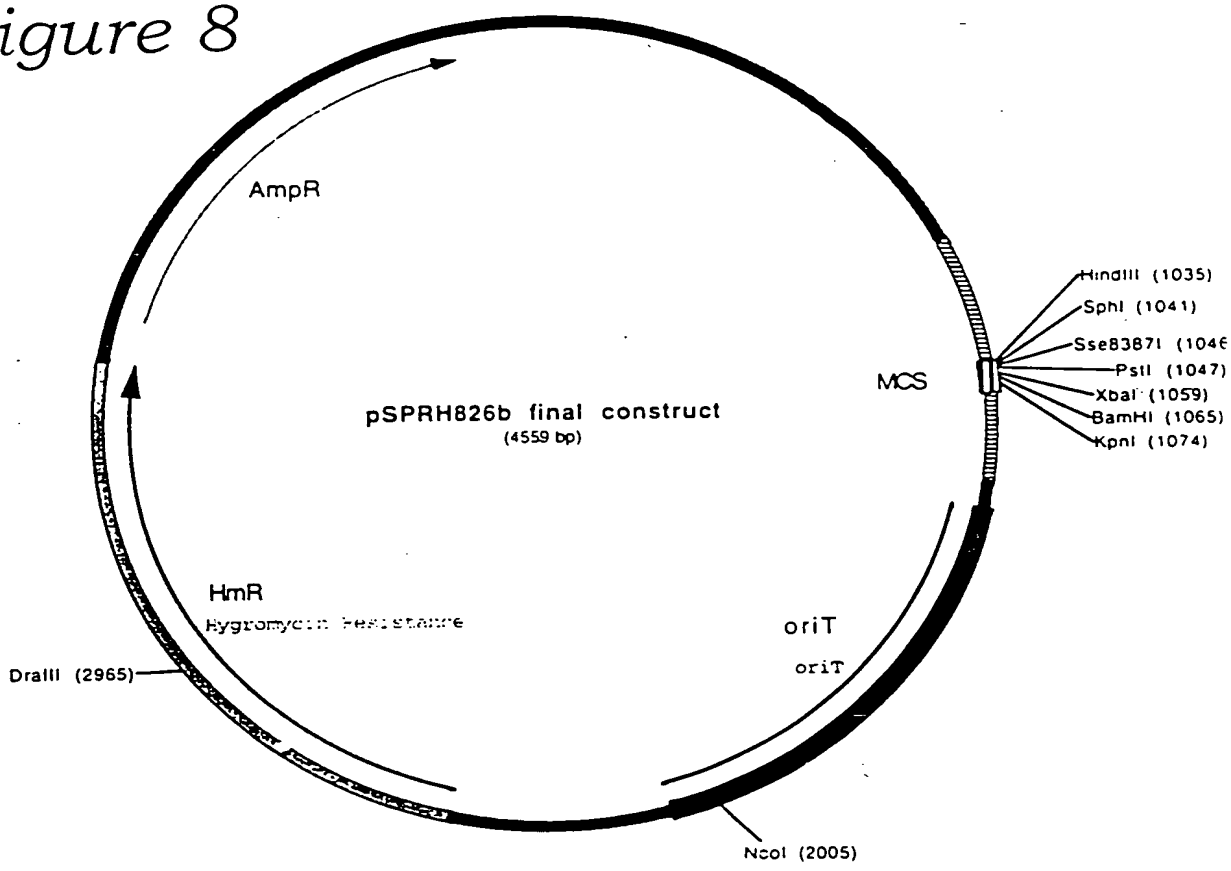

AmpR
pSPRH826b final construct
(4559 bp)
MCS
HindIII (1035)
SphI (1041)
Sse83871 (1046
PstI (1047)
XbaI (1059)
BamHI (1065)
KpnI (1074)
HmR
Hygromycin resistance
oriT
oriT
DraIII (2965)
NcoI (2005)

Figure 9

Analysis of *M. carbonacea* and *M. halophytica* pSPRH840 insertion site AttB/AttP region

A. Alignment of pMLP1 attP region with religation clone edge sequence

```
M.halophytica PstI relig-9   TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCCGGAGACGCCCCGGAGCAATCCGGA  60
M.carb PstI relig-1          TGATCAACTCTAGGGGAGGGGTAGGGGAAT-CNCTCCCGGAGACGCCCCGGAGCAATCCGGA  59
M.carb PstI relig-4          TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCCGGAGACGCCCCGGAGCAATCCGGA  60
pMLP1.intTGA.att region      TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCCGGAGACGCCCCGGAGCAATCCGGA  60
Consensus                    TGATCAACTCTAGGGGAGGGGTAGGGGAATCCNCTCCCGGAGACGCCCCGGAGCAATCCGGA  60

M.halophytica PstI relig-9   GCATGACCGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCCGGTA  120
M.carb PstI relig-1          GCATGACCGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCCGGTA  119
M.carb PstI relig-4          GCATGACCGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCCGGTA  120
pMLP1.intTGA.att region      GCATGACCGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCCGGTA  120
Consensus                    GCATGACCGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCAGGGCCCCCGGTA  120

M.halophytica PstI relig-9   CGGGTTCAATTCCCATCAGTCACCCCAGGTAAGACCCAGGTCAGGGCCGGTTCTCACC-G  179
M.carb PstI relig-1          CGGGTTCAATTCCCATCAGTCACCC---GT-ACACGAAGGCCCCCTCCAC-TCGGAGGGG  174
M.carb PstI relig-4          CGGGTTCAATTCCCATCAGTCACCC---GT-ACACGAAGGCCCCCTCCAC-TCGGAGGGG  175
pMLP1.intTGA.att region      CGGGTTCAATTCCCATCAGTCACCC---G--GCAAGTGGATCTACTCCACAGCAGATCAG  175
Consensus                    CGGGTTCAATTCCCATCAGTCACCCCAGGTARSAHSHRGRYCHVSKCCRSWKCDSABSRG  180

M.halophytica PstI relig-9   GCCCT-GACGCATTTTCAGGGG------  200
M.carb PstI relig-1          GCCTTCCGCGT-TCCTGAGGGTTCCCG-  200
M.carb PstI relig-4          GCCTTCCGCGT-TCCTGAGGGTTCCC---  200
pMLP1.intTGA.att region      GCCCCCTCCG----AAGAGGGGCCCTGAT  200
Consensus                    GCCYYCKVCGYATYHWSAGGGKKCSYGAT  209
```

Insertion juncture

B. pMLP1 attP region

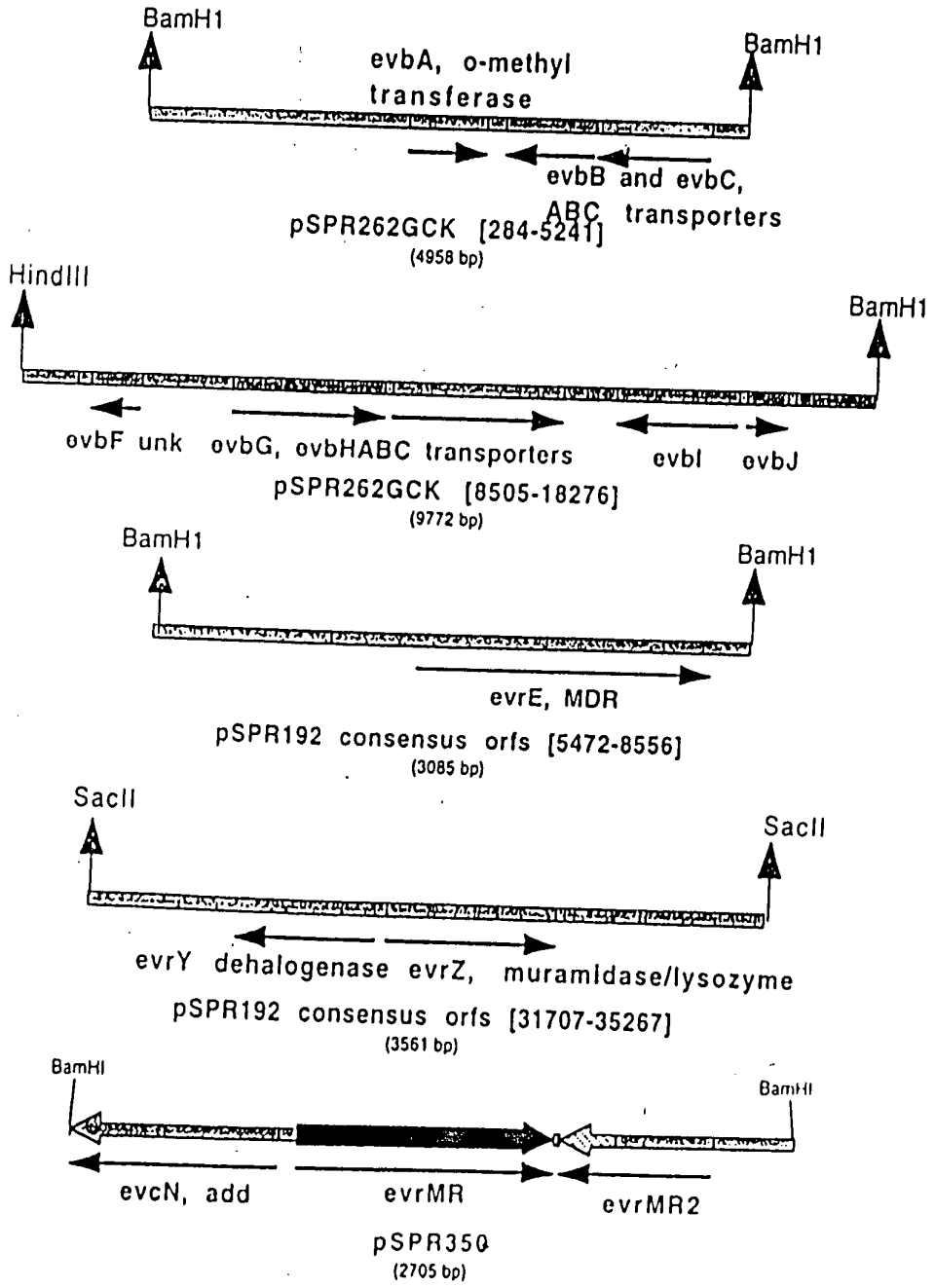
```
1   TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGGAGACGCCCCGGAGCAATCCGGAGGATGACGGAGCAACCAGCAGGTCAGGTGGCCT

94  GTTGACCCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCATCAGTCACCCGCAAGTGGATCTACTCCACAGCAGATC

174 AGGCCCCCTCCGAAGAGGGGGCCTGATGCGTCATAGGGGACAGGTAGGGGAACTCAA
```

Figure 10

Cloning scheme to test potential resistance genes



```
   1 GGTACCCGACCGTGTCCCGGAACAACGAGTCGAGATACGGCGAGAGGAACACCCCCCGGTAGTCCGGGTAGACGGTGGGCGCGAAGGCGTAC
  93 GCGCCTTCGACGGTCAGCGGGCGGGCGGACACCGGCGGGTCAGCTCGTCACGTGTACGCGGGGGACGTACAGGATCCACTGTCCGCCAGCC
                                        <  •  S  T  V  H  V  R  P  V  Y  L  I  W  Q  G  G  A
 184 CGGCGGAACTCCTGCTCCTTCGCCATGATCTCGTCGGCGTGGTTCCAGGCGAAGAGCAGCGCGTAGTCCACCGCGTCGGGCGTGAACGCGTC
    <R  R  F  E  Q  E  K  A  M  I  E  D  A  H  N  W  A  F  L  L  A  Y  D  V  A  D  P  T  F  A  D
 276 CGGGGTGCGCACCGGGATGTGCGTGCCGGGGGTGAGCCGGCCCTGCTTGGCCGGCGTCGTGTCGCACACCCAGGAGACCAGGTCCGGACCGA
    <  P  T  R  V  P  I  H  T  G  P  T  L  R  G  Q  K  A  P  T  T  D  C  V  W  S  V  L  D  P  G  I
 368 TGCCGCAGAAGTTCGTCACGGTGGCGCTCTTCGCCGTCGCGCCGTACGCCACCACCCGCTTGCCCTCGGCCTTGAGCGAGTTCAGCAGGGCG
    <  G  C  F  N  T  V  T  A  S  K  A  T  A  G  Y  A  V  V  R  K  G  E  A  K  L  S  N  L  L  A
 460 AGCAGGTCGGTGCGGATGCCCTCGACGTCGGCGGCGAACCTGTCGAGCCGGCTGCGGTCGGCGACCCCTCGGGCGTCCTCCTCGCCGATCAG
    <L  L  D  T  R  I  G  E  V  D  A  A  F  R  D  L  R  S  R  D  A  V  G  R  A  D  E  E  G  I  L
 552 CGCGGCCACCCGCTCGGCCGGCTGCCGCGCGCCGGCACGGGCGATGGTGTAGCGGACCTCCCCACCGTGCACCGGAAGGCGTTCCACGTCGA
    <  A  A  V  R  E  A  P  Q  R  A  G  A  R  A  I  T  Y  R  V  E  G  G  H  V  P  L  R  E  V  D  V
 644 CGAGCGCGAAGCCGAAGCGGGCCGCCAGCGCCTGCACCGACCGCGCCGAGAAGAAGAAGAAATGCTCGTCGTAGATCTGGTCGAAGGACGTC
    <  L  A  F  G  F  R  A  A  L  A  Q  V  S  R  A  S  F  F  F  F  H  E  D  Y  I  Q  D  F  S  T
 736 TTGTCCAGGATGTCCCCGAGGTACGGGTCCTCGAAGACGAAGACCCCGTCCGGTGCCAGCAGCGCGTCAACGCCCCGGAGGATGGAGTCGAG
    <K  D  L  I  D  G  L  Y  P  D  E  F  V  F  V  G  D  P  A  L  L  A  D  V  G  R  L  I  S  D  L
 828 GTAGGGGATGTGGCAGATGGTGTTGGCCGCGAAGATCACATCGGCGGGGCCGTCGGTCTCCCTGACCCGGCGGGCGGTGGACTCCTCGAAGA
    <  Y  P  I  H  C  I  T  N  A  A  F  I  V  D  A  P  G  D  T  E  R  V  R  R  A  T  S  E  E  F  F
 920 ACTCGGTGACCACCCGCACCCCGTGCCCACGGGCCACATCGGCCACCCCACCCGACGGCTCGAAGCCCAGGTGCCGCACTCCCGCCTCGTGG
    <  E  T  V  V  R  V  G  H  G  R  A  V  D  A  V  G  G  S  P  E  F  G  L  H  R  V  G  A  E  H
1012 ACGGTACGCAGCATCACCCCGTCGTTGCAGCCGATCTCCACCACGAACGGGTCCGGGCCGGTGGCCTCGTGCTCCAGCAGGTGCCGCGGT
    <V  T  R  L  M  V  G  D  N  C  G  I  E  V  V  F  P  D  P  G  T  A  E  H  E  L  L  H  R  A  T
1104 GTCGGCGAAGTGCTTCTGCATCACGGAGGAGCCCGACGAGTGGTACGGGTAGTCCTGGTGGAACATCTCCTCCCGGGGCACCTCCTCCATGA
    <  D  A  F  H  K  Q  M  V  S  S  G  S  S  H  Y  P  Y  D  Q  H  F  M  E  E  R  P  V  E  E  M  L
1196 GCTGCACCATCGTGCAGCCCGCGCAGACCCCCACCGCCAGGTGGAAGAAGAACTCGTCCGCGAGCTGGTCCTCGGTGAGGAACCGGTCGGAG
    <  Q  V  M  T  C  G  A  C  V  G  V  A  L  H  F  F  F  E  D  A  L  Q  D  E  T  L  F  R  D  S
1288 AGCGGCTGCCGACCCAGGTCGAGGAACTGGGCGGTGGTGCCGCCACACGCCCGGCAGGTGCCGCGCCGGGGCGTGCCGTCGGCTGAATCGGT
    <L  P  Q  R  G  L  D  L  F  Q  A  T  T  G  G  C  A  R  C  T  G  R  R  P  T  G  D  A  S  D  T
1380 CATCGCATTCCTTCCATGGATACCCCTGCCTCAGGCAGGGCGGATGTCAACGACGTCTCCTTGTCGGGATGGGTCGTCCAGCTCTCGGC
    <  M
1469 TGCGGCGTGCCGGCCGGCGACTCAGAGCGCCGCGAGCACGTCGCGCAGCGCGTCGATCACCCGGTCCTGCGTCTCCGGCGGCAGCGAGGGA
                                        <  •  L  A  A  L  V  D  R  L  A  D  I  V  R  D  Q  T  E  P  P  L  S  P
1560 TACATGGGGAGGGAGAAGATCTCGCCGGCCAACCGTTCCGTGGTGGGGAGGGAGCCGGTCTGGTAGCCGAGCTTGGCGAAGCCGGTCATGGT
    <Y  M  P  L  S  F  I  E  G  A  L  R  E  T  T  P  L  S  G  T  Q  Y  G  L  K  A  F  G  T  M  T
1652 GTGCACCGGCCAGGGGTAGCTGATGTTGAGCGCGATGTCCCGCGCCGCCAACTGTTCGAGGATGCGGTCGCGGGCGGGGTGGCGGACCACGT
    <  H  V  P  W  P  Y  S  I  N  L  A  I  D  R  A  A  L  Q  E  L  I  R  D  R  A  P  H  R  V  V  Y
1744 AGACGTACCAGACGTGTTCGTTGTCGGTCGCCGTCACCGGCAGGGTCAGGCCGACCTGGTCGGCGATGTCGGCCAGGCCCTCCTCGTAGCGC
    <  V  Y  W  V  H  E  N  D  T  A  T  V  P  L  T  L  G  V  Q  D  A  I  D  A  L  G  E  E  Y  R
1836 CGGGCCACGGCGCGGCGCCCGGCGATGTAGTCGTCGAGCCGGCACAGCTTGCGGCGCAGGATCTCGGCCTGCACCTCGTCGAGGCGGCAGTT
    <R  A  V  A  R  R  G  A  I  Y  D  D  L  R  C  L  K  R  R  L  I  E  A  Q  V  E  D  L  R  C  N
1928 GTGCCCCGGCGTCTCGACGACGTAGTAGACCTGTTCCATGCCGTAGTAGCGCAGCCGCCGCAGCCGCTCGTCGATCACGGCGTCCGCGGTGA
    <  H  G  P  T  E  V  V  Y  Y  V  Q  E  M  G  Y  Y  R  L  R  R  L  R  E  D  I  V  A  D  A  T  V
2020 CCACGCCGCCGCCGTCGCCGTACGCGCCCAGCACCTTCGTCGGATAGAACGAGAAGGCAGCGGCGTCGCCCATCGTGCCGGCCAGCCGTCCG
    <  V  G  G  G  D  G  Y  A  G  L  V  K  T  P  Y  F  S  F  A  A  A  D  G  M  T  G  A  L  R  G
2112 CCCCGACGCGCGCCGTGCGACTGCGCGCAGTCCTCCAGGACCTTGAGGCCGTGTTCCCGGGCCACCCGCAGCACCGGGTCCATGTCGACGCA
    <G  R  R  A  G  H  S  Q  A  C  D  E  L  V  K  L  G  H  E  R  A  V  R  L  V  P  D  M  D  V  C
2204 CTGGCCGTAGAGGTGCACCGGCAGCAGCGCCTTCGTCCGGGGGGTGACCGCCTCGGCCAGCAGCTCGGTGTCCATCAGGTAGTCGTCGGCGC
    <  Q  G  Y  L  H  V  P  L  L  A  K  T  R  P  T  V  A  E  A  L  L  E  T  D  M  L  Y  D  D  A  R
2296 GGACGTCCACGAAGACCGGCGTCGCGCCGACCGCGTCGATGGCGAGCACCGTCGGCGCGGCCGTGTTGGAGACGGTGATGACCTCGTCGCCC
    <  V  D  V  F  V  P  T  A  G  V  A  D  I  A  L  V  T  P  A  A  T  N  S  V  T  I  V  E  D  G
2388 GGCCCGACGTCGAGCGCCTGGAGTGCGAGCTTGATGGCGTTGGTGCCGTTGTCCACCGTGACGCAGTGCGGCATGTCGTGATAGGCGGCGAA
    <P  G  V  D  L  A  Q  L  A  L  K  I  A  N  T  G  N  D  V  T  V  C  H  P  M  D  H  Y  A  A  F
2480 CTCCTGCTCGAAGCCGCGCACGCTCGCGCCGAGGATGAGGTTCCCGGACTCGAAGACCGTCTGCACGGCGTCGAGGAGGTCGTCCCGTTCCT
    <  E  Q  E  F  G  R  V  S  A  G  L  I  L  N  G  S  E  F  V  T  Q  V  A  D  L  L  D  D  R  E  K
2572 TCTCGTACTCCGGCAGGTAGCCCCACACTCGGATGGTCATCTTCGCCCTTCTACGCCGAGGTCCGGGAGCGGAGCGCGCGCACGCTCAT
    <  E  Y  E  P  L  Y  G  W  V  R  I  T  M                    <  •  A  S  T  R  S  R  L  A  R  V  S  M
2661 GTAGTCGTTGTCCCGGTCGAGTCCAAGTGCCTGACCGCTCAGGTAGTCGACGGCGTCCACGTAGCTGTAGGGCTGCATGAACCCGCCGGCCC
    <  Y  D  N  D  R  D  L  G  L  A  Q  G  S  L  Y  D  V  A  D  V  Y  S  Y  P  Q  M  F  G  G  A  R
2753 GCACGTCGCGATAGAGCCGGGAGAGTGGGTGCCCGGCCGTGTAGGCGAGGCCGCCGACCAGGCTGAGGCAGTCGTCCACCACCGCCGGGGCC
    <  V  D  R  Y  L  R  S  L  P  H  G  A  T  Y  A  L  G  G  V  L  S  L  C  D  D  V  V  A  P  A
2845 AGCTCGTTGACGGTCATCTTCGCGTACTGGAACGGGGTCATCATCCGTCGGCCGCGTTCGTCCGGGTCGCCGGACAGGTCGACCGACGCCGC
    <L  E  N  V  T  M  K  A  Y  Q  F  P  T  M  M  R  R  G  R  E  D  P  D  G  S  L  D  V  S  A  A
2937 GTCGGCGTTGGTCAACGCCGCGCCGACCGTGGTGCGTAGCGCGTAGAGCCGGGTGTCCAGCCCGGCGACCAGCGCCCGGGCACCGGCCCGTG
    <  D  A  N  T  L  A  A  G  V  T  T  R  L  A  Y  L  R  T  D  L  G  A  V  L  A  R  A  G  A  R  P
3029 GCTCGCCGCCGCGCCCCGCGCAGAAACCGACCGCGATGTCCCGGGCCGCCTGGGCGATGCCGGCGTAGATGCCGAGCATGGTGATCGAGCTG
    <  E  G  G  R  G  A  C  F  G  V  A  I  D  R  A  A  Q  A  I  G  A  Y  I  G  L  M  T  I  S  S
3121 ACCGTCTGCCCGGCCAGCACGGCGTCCCGCCGGGCCCCGACCGGGCCGCGCTCCAGCAGCTCGTCGGCCCGGACCGGGCACCGGTCGAAGAC
    <V  T  Q  G  A  L  V  A  D  R  R  A  G  V  P  G  R  E  L  L  E  D  A  R  V  P  C  R  D  F  V
3213 CACCTCCAGCGTCCCCGAGGCACGCATTCCCAGGCCGTCCCAGTTGTCCAGCACCGTGAGCCCGGGGGCGTCGCGGTGCACGACCGGCACGG
    <  V  E  L  T  G  S  A  R  M  G  L  G  D  W  N  D  L  V  T  L  G  P  A  D  R  H  V  V  P  V  A
3305 CGAGGAACACCGAGCCGTCGTCGTCGCGCCGCTGGGCGTGCACGAAGAAGTGGGTCGCGATGGGCGCCATGCTGACCAGCACCTTGCGGCCC
    <  L  F  V  S  G  D  D  D  R  R  Q  A  H  V  F  F  H  T  A  I  P  A  M  S  V  L  V  K  R  G
3397 GACAGCAGCCAGCCGCCGGCGCCGTCGGAATGCAGCTCGGTGACCACGCCGGGGGCGTCCTTGAGCGCGCCGCAGACGGCGGCCTCGCCCTC
    <S  L  L  W  G  G  A  G  D  S  H  L  E  T  V  V  G  P  A  D  K  L  A  G  C  V  A  A  E  G  E
3489 CGCCATCGCCCGCAGCAGCCGCTCCGCCATCGCGCGCACCGGCGGCGTGCCGTGCTGCCACTCGTAGGTGAGGGTGAGGCCCCGGCTGAGCT
    <  A  M  A  R  L  L  R  E  A  M  A  R  V  P  P  T  G  H  Q  W  E  Y  T  L  T  L  G  R  S  L  Q
3581 GCACGTGCCAGGCCAGCGCGGTGGACGCGTCGGCCTCGGCCAGCCGCATCAGCGCGGTCGCCACGTCGTACAGCCGGGTCAACCCCAGGCCG
    <  V  H  W  A  L  A  T  S  A  D  A  E  A  L  R  M  L  A  T  A  V  D  Y  L  R  T  L  G  L  G
```

Figure 11A

```
3673 CCCAGCTCGGCGGGAACGGTGGCGCCCATCAACCCGAGCTTCGCGAACTGCTCGAACGCCTCCACCGGGAAGGTGCCGGTGCGGTCCCGGTC
    <G  L  E  A  P  V  T  A  G  M  L  G  L  K  A  F  Q  E  F  A  E  V  P  F  T  G  T  R  D  R  D
3765 GGCGGCCTCCGCACTGATTCTCGGGATCACGCCGGCAAGCAGGTCGACCACCGTGCGCCCCCGCCGGCGTGAGCGGCGCGCGAAGATCCGCCG
    <A  A  E  A  S  I  R  P  I  V  G  A  L  L  D  V  V  T  R  G  A  P  T  L  P  A  R  L  D  A  A
3857 CCACCCATCTCTCCTCGGTCAGATTAGACATCGCCTGCTTCCGTTCGCGCTGTGCCGAACCTGTCGCTATCAGGGTGCGCGGCGATCACC
    <  V
3947 AATTGCTGGCTGATTGTCCACCGACGATGCTCGACAGGGATACCCAGAATAGGCGGCAACGGCTTGGCGAAACCCCTGTCGTGCGCCGGAGT
4039 TCGCCAAGTCTAGTTGGATCACTCGAGCTTCCCCCGCAGAAGCCGTGAACCATGGGCCAGCGGTTGACGTCGCTATATATTCGGCCGACACG
4131 TGCGGAGGACTCGTGAAGATACTGTTCATCGCAGGACCGACGAAGTCCAGCCTATTCGGCCTGGCCCCACTGGCAATCGCCGCCCGGATG
                >V  K  I  L  F  I  A  G  P  T  K  S  S  L  F  G  L  A  P  L  A  I  A  A  R  M
4221 AGCGGGCACGAGGTCGTGATGGCTTCCACGCAGGAGGTCGTACCGGCGACGATGTCCGTCGGGCTGCCGGCCTTCCCGCTGGCGGCGCTGAC
    >S  G  H  E  V  V  M  A  S  T  Q  E  V  V  P  A  T  M  S  V  G  L  P  A  F  P  L  A  A  L  T
4313 CCTCGCCGAGCTCATGACCACCGACCGGGCCGGCGATCCGCTGCGCATCCCGGCCGAGGACGCCGCCTTCGTCCCCTTCGTCGGCCGGATGT
    >L  A  E  L  M  T  T  D  R  A  G  D  P  L  R  I  P  A  E  D  A  A  F  V  P  F  V  G  R  M
4405 TCGGCCGGCTGGCGGCGATCAGCCTGGATCCGCTGCGCGACCTGGTCGGCGGGTGGCGGCCCGACCTGATCGTCGGCGGCCCGCACGCCTAC
    >F  G  R  L  A  A  I  S  L  D  P  L  R  D  L  V  G  G  W  R  P  D  L  I  V  G  G  P  H  A  Y
4497 GCCGCGCCGATCCTGGCCACCGAACTTGGGGTGCCCTGCGTGCGGCACCTGCTCACCGGCAACCCGGTGGACCGCGAGGGCACCCATCCGGG
    >A  A  P  I  L  A  T  E  L  G  V  P  C  V  R  H  L  L  T  G  N  P  V  D  R  E  G  T  H  P  G
4589 GGTCGACGAGGAGCTGCGGCCGGAGCTGGCCGCGCTCGGCCTGGCCCAGGTGCCGCCGTTCCACCTGGCCCTGGACATCTTCCCGGCCAGCA
    >V  D  E  E  L  R  P  E  L  A  A  L  G  L  A  Q  V  P  P  F  H  L  A  L  D  I  F  P  A  S
4681 CCCGGATCGACGACGTCCCGCCGGCGCAGCCGGTGCGACCGCTGCGCTGGATTCCGACCAACCAGCAGCAGCCGGTGGCGCCGTGGATGCTC
    >T  R  I  D  D  V  P  P  A  Q  P  V  R  P  L  R  W  I  P  T  N  Q  Q  Q  P  V  A  P  W  M  L
4773 TCGCGCGGGCCGCGTCGCCGTGTCCTGGTCACCGCCGGCAGTCTGGTCACCACCACCCACAACTTCGACTTCCTCCACGGACTGGCCGGCAC
    >S  R  G  P  R  R  R  V  L  V  T  A  G  S  L  V  T  T  T  H  N  F  D  F  L  H  G  L  A  G  T
4865 CCTGGCCGAGCAGGACGTCGAGGTCGTGGTCGCGGCGCCGCCGGAGGTGGGTCGGGCCCTGCACGACGTGCCGGGTGTGCGGCACGCCGGCT
    >L  A  E  Q  D  V  E  V  V  V  A  A  P  P  E  V  G  R  A  L  H  D  V  P  G  V  R  H  A  G
4957 GGCTCCCGCTGGACGTGGTGCTGCCCCACTGTGACCTGATCGTGCACCACTCCGGCACGATGACCGCGCTGACCGCCTTGAACGCGGGGGTG
    >W  L  P  L  D  V  V  L  P  H  C  D  L  I  V  H  H  S  G  T  M  T  A  L  T  A  L  N  A  G  V
5049 CCCCAGCTGATCGTGCCGCAGGAGAGCCGGTTCATCGAGTGGGCGCGCAACCTGTCGACCCTGGGCGTGGCGCAGACCCTCGCGCCGGGCGA
    >P  Q  L  I  V  P  Q  E  S  R  F  I  E  W  A  R  N  L  S  T  L  G  V  A  Q  T  L  A  P  G  E
5141 GGACACGCCGGAGGCCGTGGGCAAGGTCGCCCGCCTGCTGCTGGAGGATCCGGTCCACGCCACCAGCGCCGCCGCGATCGCCCGGGAGATCG
    >D  T  P  E  A  V  G  K  V  A  R  L  L  L  E  D  P  V  H  A  T  S  A  A  A  I  A  R  E  I
5233 CCGAGATGCCCGGCCCCACGGAGGTCGTGGGCCAGCTCACCGAGTTCGCGACCCGGGGCCTGACATGCGCGTCCTCGTGACCGGCGGAGCC
    >A  E  M  P  G  P  T  E  V  V  G  Q  L  T  E  F  A  T  R  G  L  T  C  A  S  S  •
                                                                                    >V  T  G  G  A
5324 GGGTTCATCGGCTCCCACCTCACCGACGCGCTGCTCGAACGCGGCGACAGCGTCACCGTGCTCGACGACCTGTCCACCGGGCGGCCCGAGCG
    >G  F  I  G  S  H  L  T  D  A  L  L  E  R  G  D  S  V  T  V  L  D  D  L  S  T  G  R  P  E  R
5416 GCTGCCCGCCGGGGTGCCGCTGCACCACGGGTCGATCACCGACCGGGCCGGGTTGACCCGGCTGGCCGAGCAGTGTCGCCCGGAGGTCATCT
    >L  P  A  G  V  P  L  H  H  G  S  I  T  D  R  A  G  L  T  R  L  A  E  Q  C  R  P  E  V  I
5508 GCCACCTGGCCGCCCAGGCGGACGTGCGCAACTCGGTGGCCGACGCCACCTCGGACACCGGGGTCAACGTGGTCGGCACCGTCAACGTCCTG
    >C  H  L  A  A  Q  A  D  V  R  N  S  V  A  D  A  T  S  D  T  G  V  N  V  V  G  T  V  N  V  L
5600 GAGGCCGCCCGGGCCATCGACGCCCGGGTGGTCTTCGCCTCCAGCGGCGGCGCCCTCTACGGGGAGGTCGACGAGCTGCCCTCCCCCGAGGA
    >E  A  A  R  A  I  D  A  R  V  V  F  A  S  S  G  G  A  L  Y  G  E  V  D  E  L  P  S  P  E  D
5692 CGTCCGGCCGGCGCCGTGGGCGCCGTACGGGGCCGCCAAGTACTGCGCGGAGCAGTACCTGGCGCTCTACAACCGGCTCTACGGCTCGACCC
    >V  R  P  A  P  W  A  P  Y  G  A  A  K  Y  C  A  E  Q  Y  L  A  L  Y  N  R  L  Y  G  S  T
5784 ACGCGGCGCTGCGGCTCGGCAACGTGTACGGGCCACGCCAGGACCCGACCGGCGAGGCCGGGGTCGTCTCGATCTTCTGCGGCTGCCTGGTG
    >H  A  A  L  R  L  G  N  V  Y  G  P  R  Q  D  P  T  G  E  A  G  V  V  S  I  F  C  G  C  L  V
5876 GCCGGGCGCCGGCCGACGGTGTTCGGCGACGGCGAGCAGACCCGGGACTACATCTACGTGGCCGACGTGGTGGAGGCGTTCCTGCTCGCGGT
    >A  G  R  R  P  T  V  F  G  D  G  E  Q  T  R  D  Y  I  Y  V  A  D  V  V  E  A  F  L  L  A  V
5968 CGGGCACGGTGGCCCCGGCCTGTGGAACATCGGCACCGGGACCTCCACCAGCATCCGCAAACTACTGGACCTGGTCGGCCGCACCGCCGGGC
    >G  H  G  G  P  G  L  W  N  I  G  T  G  T  S  T  S  I  R  K  L  L  D  L  V  G  R  T  A  G
6060 GCGTCCCGGACCCCCGCTTCGAGCCACCCCGCCTGGGCGAGCTGAAGCACTCCGCGCTGGAGGTGACCCGCGCGGCCCGGGAGCTGCGCTGG
    >R  V  P  D  P  R  F  E  P  P  R  L  G  E  L  K  H  S  A  L  E  V  T  R  A  A  R  E  L  R  W
6152 GCGGCCCGAACGAGGCTCGCCGACGGCATCGCGAAGGTCTACAAGTGGGTCGAGGCGGACGAACCGGTCCGGGGGGAGCGATGACCCGCG
                                                                                    >M  T  R
    >A  A  R  T  R  L  A  D  G  I  A  K  V  Y  K  W  V  E  A  D  E  P  V  R  G  E  R  •
6242 AGGGGTCAACGCCGCCGGTTAGGGTCGCCACCATCACGGTCGGCACCAACGAGATCCGTTGGCTGGACCGCGCGCTCGGCTCGCTGCTCGCC
    >E  G  S  T  P  P  V  R  V  A  T  I  T  V  G  T  N  E  I  R  W  L  D  R  A  L  G  S  L  L  A
6334 AGCGACACGACCGGCTTCGAGCTGACGGTCTTCTACGTGGACAACGCCTCGGCCGACGGCAGCGTGGCGCACGTCATGTCGGCGTTTCCCGG
    >S  D  T  T  G  F  E  L  T  V  F  Y  V  D  N  A  S  A  D  G  S  V  A  H  V  M  S  A  F  P  G
6426 CGTCCGGGTCATCCGAAACCCCCGCAATCTCGGCTTCACCGGCGCGAACAACGTCGGCATGCGGGCGGCCCTGGCGGAGGGCTTCGACCACA
    >V  R  V  I  R  N  P  R  N  L  G  F  T  G  A  N  N  V  G  M  R  A  A  L  A  E  G  F  D  H
6518 TCTTCCTGGTCAACCCGGACACCTGGACACCGCCGGGGCTGGTCCGCGGGCTGGTCGAGTTCGCGCAGCGGTGGCCGCAGTACGGCGTCATC
    >I  F  L  V  N  P  D  T  W  T  P  P  G  L  V  R  G  L  V  E  F  A  Q  R  W  P  Q  Y  G  V  I
6610 GGCCCGTTGCAGTACCGCTACGACCCGGCGTCGACCGAGTTGACCGACTTCAACGACTGGACGCAGGTCGCCCTCTACCTGGGCGAGCAGCA
    >G  P  L  Q  Y  R  Y  D  P  A  S  T  E  L  T  D  F  N  D  W  T  Q  V  A  L  Y  L  G  E  Q  H
6702 CACCTTCGCCGGCGACCTGCTGGATCATCCCTCGCACGTCACCGCGACGGTCCGCGACCGCGCGCCGCGCACCCTGGAGCACGCGTACGTGC
    >T  F  A  G  D  L  L  D  H  P  S  H  V  T  A  T  V  R  D  R  A  P  R  T  L  E  H  A  Y  V
6794 AGGGCTCGGCGCTGTTCGTCCGGGCCGCCGTGCTACGCGAGGTCGGCCTGCTCGACGAGGTGTTCCACACCTACTACGAGGAGGTCGACCTG
    >Q  G  S  A  L  F  V  R  A  A  V  L  R  E  V  G  L  L  D  E  V  F  H  T  Y  Y  E  E  V  D  L
6886 TGCCGGCGGGCCCGGTGGGCGGGCTGGCGGGTGGCGCTCCTACTCGACCTCGGCATCCAGCACAAAGGCGGCGGTGGCACCGCCGCGAGCGC
    >C  R  R  A  R  W  A  G  W  R  V  A  L  L  L  D  L  G  I  Q  H  K  G  G  G  G  T  A  A  S  A
6978 GTACAGCCGGATACACATGCGCCGCAACCGCTACTACTATCTGCTGACCGATGTGGACTGGCCCCCGGCCAAGGCCGCCCGGCTCGCCGCCC
    >Y  S  R  I  H  M  R  R  N  R  Y  Y  Y  L  L  T  D  V  D  W  P  P  A  K  A  A  R  L  A  A
7070 GCTGGCTGTTCTCCGACGTCCGTGGGCGGGGCGTGACGGGTCGGACGAGCGCGGGCGTCGGGGCGCGGGAGACCTTCGTGGCGCTCGGGTGG
    >R  W  L  F  S  D  V  R  G  R  G  V  T  G  R  T  S  A  G  V  G  A  R  E  T  F  V  A  L  G  W
7162 CTGGCCCGCCAGGCCCCGGTGATCCGGGAACGTCGTCGGCGGCACCGGCTGCTGCGGGCACGAGGGACGGGCGTGGACCGCGCCCGAGAGCG
    >L  A  R  Q  A  P  V  I  R  E  R  R  R  R  H  R  L  L  R  A  R  G  T  G  V  D  R  A  R  E  R
```

Figure 11B

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7254 GAAGGAAACCGTGCGGGGATGAGCAGGCCACGGATTCTCGTCGCGGGCAACTTCCACTGGCAGGCCGGGTTCAGCCAGACCGTCGCCGCGT
    > K E T V R G ∘
                        > M S R P R I L V A G N F H W Q A G F S Q T V A A
7345 ACGTGCGGGCGGCCCGGGAGGCCGACTGCGAGGTGCGGCTCTGCGGCCCGCTGTCCCGGGTCGACGCCGAGACGGCCCGGCACCTGCCGGTC
    >Y V R A A R E A D C E V R L C G P L S R V D A E T A R H L P V
7437 GAGCCGGACCTCCGCTGGGGCACCCACCTGGTGATCATGTTCGAGGCCAAGCAGTTCCTCACCGAGGCGCAACTGGACCTCGTCGAGGCGTT
    > E P D L R W G T H L V I M F E A K Q F L T E A Q L D L V E A F
7529 CCCCCGACAGCGCCGGGCCATCGTCGACTTCGACGGGCACTGGGGTGCCGAGGAGGGCGGGGACGGCGACAGCGCGTCGGGCCGGTACTCCG
    > P R Q R R A I V D F D G H W G A E E G G D G D S A S G R Y S
7621 CGGAGAGTTGGCGGCGGTTGTACTCGACCCTGAGCGACCTGATCCTGCAACCCCGGCTGGGTCCGCTCCCGGCCGGCGCCCGGTTCTTCAAG
    >A E S W R R L Y S T L S D L I L Q P R L G P L P A G A R F F K
7713 TGCTTCGGCCTGGCAGCGCCGGTGCGGCACCCGCTGGAACTGGGCACCGGCGCGCAGTCGCGCCCGTACGACCTCCAGTACATCGGCAGCAA
    > C F G L A A P V R H P L E L G T G A Q S R P Y D L Q Y I G S N
7805 CTGGTGGCGGTGGGAGCCGATGACCGAGATGGTCGAGGCCGCGGCGGCGGCCCGGCCGCCGCTGCGCCGGCTGCGGGTGTGCGGACGCTGGT
    > W W R W E P M T E M V E A A A A A R P P L R R L R V C G R W
7897 GGGACGGCGGCAGTTGCGCGGGCTTCGAGGAGGCGACGCTCAGCGAGCCGGGCTGGCTGCGGGCGCGCGGCGTCGAGGTGCATCCGCCCGTG
    >W D G G S C A G F E E A T L S E P G W L R A R G V E V H P P V
7989 CCGTTCGGCCACGTGGTCGAGCAGATGGGCCGGTCGCTGATCTCACCGGTCCTGGTGCGGCCGCTGGTCACCAGCACCGGCCTGTTGACCCC
    > P F G H V V E Q M G R S L I S P V L V R P L V T S T G L L T P
8081 CCGGATGTTCGAGACGCTGGCCTCGGGCAGCCTGCCCGTGCTCCCGGTCGCCGCGAAGTTCCTCGCGCCGGTCTACGGCGACGAGGCGGAAC
    > R M F E T L A S G S L P V L P V A A K F L A P V Y G D E A E
8173 ACCTGATGCTCGGCGACGACCCGGCCGGAACGCTGAGCCGGCTCTCGGCCGAGCACGAACGGTACGGACGACTGGTCGGTGAGATTCAGGAC
    >H L M L G D D P A G T L S R L S A E H E R Y G R L V G E I Q D
8265 CGGCTCCGCGTCGAGTACGGCTACCCTCGCGTCCTGCGGGACCTGCTCGATCTGCTGGCCTGAGGAATGAGGAGCAGATGACCCCCCTG
                                                        > M T P L
    > R L R V E Y G Y P R V L R D L L D L L A ∘
8354 CGGATCGCGATGGTCAACATACCGTTCCGGTTGCCGAGCGACGAGCGGCAGTGGATCACGGTCCCGCCGCAGGGGTACGGCGGGATCCAGTG
    > R I A M V N I P F R L P S D E R Q W I T V P P Q G Y G G I Q W
8446 GATCGTGGCCAACAAGATCAAGGGCCTGCTCGAACTCGGGCACGAGGTGTTCCTGCTCGGTGCCCCGGGCAGTCCGCGTACGCATCCACGCC
    > I V A N K I K G L L E L G H E V F L L G A P G S P R T H P R
8538 TGACCGTGGTGCCGGCGGGCGAGCCCGAGGACATCCGGGCATGGTTGAAGTCCGCTCCGGTGGACGTCGTCAACGACTACAGCTGCGGCAAG
    >L T V V P A G E P E D I R A W L K S A P V D V V N D Y S C G K
8630 GTGGATCCGATCGAGCTGCCCCCGGGGGTCGGCCTGGTGGCCTCGCACCACATGACCACCCGCCCGTCCTATCCGGCCGGCTGCGTGTACGC
    > V D P I E L P P G V G L V A S H H M T T R P S Y P A G C V Y A
8722 CTCGAAGGCGCAGCGGGAGCAGTGCGGCGGCGGCGCGGACGCCCCGGTCATCCCGATCGGGGTGGATCCGTCGCTCTACCGCCCCGGCGACC
    > S K A Q R E Q C G G G A D A P V I P I G V D P S L Y R P G D
8814 GCAAGGACGACTTCCTGCTCTTCATGGGCCGGATCTCCCCGTTCAAGGGCGCGCTGGAGGCGGCCGCGTTCGCCCGGGCCGCCGGCCGCCGG
    >R K D D F L L F M G R I S P F K G A L E A A A F A R A A G R R
8906 CTACTGATGGCCGGTCCGGCCTGGGAGCCGGAGTACCTCGACCGGATCATGGGCGAGTACGGCGACCACGTCACCCTCGTCGGCGAGGTGGG
    > L L M A G P A W E P E Y L D R I M G E Y G D H V T L V G E V G
8998 GGGTCAGGAACGTATGGACCTGCTCGCCACGGCGGCTGCCATCCTGGTGCTCTCCCAGCCGGTGCCCGGCCCGTGGGGCGGCACGTGGTGCG
    > G Q E R M D L L A T A A A I L V L S Q P V P G P W G G T W C
9090 AGCCGGGTGCGACCGTGGTGTCCGAGGCGGCGGCCAGCGGCACCCCGGTGGTCGGCACGAGCAACGGCTGCCTGGCGGAGATCGTGCCGGCC
    >E P G A T V V S E A A A S G T P V V G T S N G C L A E I V P A
9182 GTCGGCGAGGTGGTGGGCTTCGGCACCGGCTTCGACGAGCGGGAGGCCCGAGCGGTGCTGTCCCGACTGCCGTCGCCCGCCCAGGCGCGGAA
    > V G E V V G F G T G F D E R E A R A V L S R L P S P A Q A R K
9274 GGCCGCGATCCGGTGCTGGGGGCACGTGGAGATCGCCCGGCGCTACGAGGCGGTGTACCGCGACGTGCTGGCCGGCGCGCGCTGGTCCTGA
    > A A I R C W G H V E I A R R Y E A V Y R D V L A G A R W S ∘
9365 GCCGGCCCGGGCGGCGGCTACGGTCGCGACCGTAGGGGGTGCCCGCCGCACGCGGAAGCGCCGGTGTCGGCGGTCCGACACCGGCGCGCCCG
9457 GCCAGGTCAGCTCCGGTCGTGCAGCCAGGGTCGCGGCTCGGGGTCGGTCACCTCGACCGGCTGGCTCATGAACACCAGGACGTACGCGCGG
        < ∘ S R D H L W P R P E P D T V E V P Q S M F V L V Y A R
9548 CGCGGCTGGTCCGTCTCGTTCGGGCCGGCGTAGTGCGGCGCACGGAAGTCGTGCATGACCGCCTCGCCCGGCCGCAGCGGGCAGGCGACGCT
    <R P Q D T E N P G A Y H P A R F D H M V A E G P R L P C A V S
9640 GTCCGTGTCGTCGACCTCGTCCGTCATCAGACCTTCGATGCGGTCGTCGTGGTTGATGTGATGGTGCGGGAGCACCCCGCCCCGGTCGAGGC
    < D T D D V E D T M L G E I R D D H N I H H H P L V G G R H L G
9732 CCGGCAGGTACTGGAGACAGCCGCTGGACACCGTCGCCTCGTCGAGCGGGGTCCAGATGCTCAGGCCGCGACGGGACCAGCGCGGGTCCATG
    < P L Y Q L C G S S V T A E D L P T W I S L G R R S W R P D M
9824 TACGCCTCGTCCTGGTGCCACGGAGTGGGTGCGCCGTAGCGCGGCGGCTTGAGGATCGCGTGGCCGTAGAAGTCGAGTTCGTCCTCGGGGAT
    <Y A E D Q H W P T P A G Y R P P K L I A H G Y F D L E D E P I
9916 GTCGAGGAAAGCGGAGGCGATGGCCCGGCATCGCGCGAAGTGCGCGGTCTCCACCAACTCCGGCAGGTATTTCTCCGGCCGGACGATCTGCG
    < D L F A S A I A R C R A F H A T E V L E P L Y K E P R V I Q P
10008 GGAGACGGGCAGGCGCGGCGTCGTCGCCACGGCCGGCGATGTCCCGGTAGTCGCCGGTGTCGGGCGACGCGTGATCGGCGAAGAGCCGGTCG
    < L R A P A A D D G R G A I D R Y D G T D P S A H D A F L R D
10100 TAGGCGGCCCGGAGCCAGGCGACCTCGGCGTCGTCGGCGAGCTGCGGGAGAGTCACGAAGCCATCGCGCCGGTAAGCCTCCAGCCGACGGTC
    <Y A A R L W A V E A D D A L Q P L T V F G D R R Y A E L R R D
10192 GACGACCTCCGCACCAACAGTCCCCACGGCCATTTGACCACCTCTCGGAATAGCCTGTCCGCGAATAAACCATACGGTAGGAACAGCGCG
    < V V E A G V T G V A M
10282 GCGATACCGCTCCCGAGCGGGAAATAGGGATTCGACTAGTATTCGGTCCGCGCCGCTGCCAGAACGGCACGCGCTCTCGATTGTCCATTCAT
10374 CCCCGTGCGAGACTCGCCTCGATGTCCTCGATGTCGGTGGGGGGTTTGGGATGACCGGGCACAGCGCCGTCGCGCTGGACGTCGGCGGGGT
                                                        > M T G H S A V A L D V G G V
10465 CGTCTACTACGACGAGCCGTTCGAGCTGGCCTGGCTCCAGGACACCTTCGACCGCCTCCAGGCCACCGACCCGACGCTCGACCTGCGTGCGT
    > V Y Y D E P F E L A W L Q D T F D R L Q A T D P T L D L R A
10557 TTCTGGAGCACGTCGAGCGGTTCTACCACTACGGCGAGGGCGACCCAACCGGCCGGACCTGGCTCCACTCGGAGGCCGCCGCGCTGAGCTGG
    >F L E H V E R F Y H Y G E G D P T G R T W L H S E A A A L S W
10649 TCGCGGGTCCGGCAGTCCTGGGGCGAGCTGGCCCAGGAGATTCCCGGTGCCGTTCGCGCGGTCACCAGGCTGGCCAGGGAACTACCCGTCGT
    > S R V R Q S W G E L A Q E I P G A V R A V T R L A R E L P V V
10741 GATCGTCGCCAACCAGCCCCCCGAGTGCGCGGACGTACTGGCCCGGTGGCAGGTCAGCCAGGTCTGCCGGGAGGTGCTCCTCGACTCCCTCG
    > I V A N Q P P E C A D V L A R W Q V S Q V C R E V L L D S L
```

Figure 11C

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10833 TCGGGGTGGCCAAGCCCGACCCGGCCCTGCTCGGGCTCGCCCTGCGGCGGCTGGCGATCCCGCCCGCCGAGTTGCTGGTGGTGGGCAACCGG
     >V G V A K P D P A L L G L A L R R L A I P P A E L L V V G N R
10925 ACGGATCACGACGTCCTGCCCGCGCTCGGGCTCGGTTGCCCGGTGGCGTTCGTGCTGCCCGATCCGGCGTACCGCCGGCCGCCGGGCGTCCA
     > T D H D V L P A L G L G C P V A F V L P D P A Y R R P P G V H
11017 TCCGGACCTGGTCCGGGTCTACACGGAGCTGAGGGCGTTCCGCACCGGCTCCCCGCCCGCGGACGCCCGGGTCACCACCGTGGCGTCCCTGG
     > P D L V R V Y T E L R A F R T G S P P A D A R V T T V A S L
11109 CGGCCCTGGCCGACTCTCCCCTGACGAGTGCCACCCCGCGTTCGAACGCCGGCACCGGCGGACTTTGACGAAGGAGTGCAGTTGCGACGCC
     >A A L A D S P L T S A T P R S N A G T G G L •
11200 CCGCAGCGGTGGTCGGCGCCACCGGCTTCATCGGCTCACGCCTCGTCTCCCGCCTGGCCGAGGCCGGGCATCCGGTGGCGCGCTTCAGCCG
11291 TGCCGCCCCACCCGTCGTCGACGGCCGGCCCGCGCCGGGGCTCCGCGAGGCGCAGGTCGTCTACTTCCTCGCCGCCCGGCTGAGCCCGGCGC
11383 TGGCGGAGCAGCAACCGGAACGGGTCGTCCGGGAACGCGAGTTGTTGCTGGACGTGCTAAGTGCGCTGGCGGGGGTGGACCACCGGCCGGTG
11475 TTCGTCCTGGCCAGCTCGGGCGGGGCGGTGTACACGCCGACGGTGTGGCCGCCCTACCACGAGCGGTCGGCCACCGGGCCCGCCTCGGCGTA
11567 CGGCCGGGCGAAGCTGCGGCTGGAACAGGAGCTGCTGCGCCACACCGACCGGGTGCAGCCGGTGGTGACCCGGCTGAGCAACGTCTACGGTC
11659 CGGGGCAGCGGCCGACCCCCGGGTACGGTGTCCTGTCACACTGGCTGGAGGCCACCGTGCGCGGAGAGCCGATCCGGCTCTTCGGCGATCCG
11751 GCCGTGGTGCGGGACTACGTACACGTCGACGACGTCACCGCGATCATGGAGGTCATCGCGCAGCGGGCCGGTGACGGCGACCGGGACCGGCT
11843 GCCCACGGTCGTGAACGTCGGCTCGGGCCTGCCCACCTCCCTCGCCGAGTTGCTCCAGACGATGTCCACGGTGGCCGGTCGTGAGCTGGAGG
11935 TCATCCGGGACGTCCGCCGGCAGTTCGACCATCGGGGCAACTGGCTCGACACCACCCTCGCCCGGGAGACCCTGGGCTGGCAGGCGCGGATC
12027 AGCCTCCCCGACGGCGTCCGCCAGTGCTGGGAGGCCGTCCTCACCCGGGCGGGCGGCCCGGGGGGTTCCCCGGCCCGACCGTCAGCCCGGC
     > S L P D G V R Q C W E A V L T R A G G P G G S P A R P S A R
                                                          < • G P
12118 TCGGGAGAGCGTCTCGGGGGCGGGAACCGCCGCAACCGCGCCCTTCGCAGCAGTTCGTGGCTCAACCCGGCGGCGGTCGCCGCGGTGTAGCC
     >L G R A S R G R E P P Q Q P R P S Q Q F V A Q P G G G R R G V A
     <E P S R R P P P F R R L R A R R L L E H S L G A A T A A T Y G
                                                          junction marker
12210 GAGGGCCAGTGGCAGGGCGAGCCGGGATTCCGGGGCCGTACGGTGCCGGTCCCATTCCTTGCGCAGGCCGGCCCGTGCCTGGTTCCGTCCGG
     > E G Q W Q G E P G F R G R T V P V P F L A Q A G P C L V P S G
     < L A L P L A L R S E P A T R H R D W E K R L G A R A Q N R G A
12302 CCTCGCACCGCCCCTGCCAGTACGCCCGCCGCAGCAGGTACCGGGGGGTCAGCCGGCCCGGGTCGATGTCATGGGTGACC
     > L A P P L P V R P P Q Q V P G G Q P A R V D V M G D
     < E C R G Q W Y A R R L L Y R P T L R G P D I D H T V
12382 GCGTGGTCCGGGAGCAGTTGCTCGCGGGCGCCGGCGGCCTTCATGGCGCTGATGAAGGAGGTGTCCTCC
     >R V V R E Q L L A G A G G L H G A D E G G V L
     <A H D P L L Q E R A G A A K M A S I F S T D E
12451 CCTGACTGGAGGTTGCCCCCGGTACGGCTGAGGGCCAGGTCGAAATCCAACCCGTGGGCGTGCGCGAAC
     >P •
     <G S Q L N G G T R S L A L D F D L G H A H A F
12520 GCGGAGTCCACCCCCATGCACGCGCCCCAGATCTTGATGTTTCCCTGGTCACGGTGCCAGCCGACCAGGTGGAACTGGCCGGA
     <A S D V G M C A G W I K I N G Q D R H W G V L H F Q G S
                                   junction marker
12603 GGTGACGTACCACGGCAGACGCAGCGCGGGGCGGGCCAGCCGGGTGCCGACCACGTGCGCGCCGTCGCGCAGGCTCTTGCGGACGGCGTCGA
     < T V Y W P L R L A P R A L R T G V V H A G D R L S K R V A D V
12695 CGGCAGCGGCGTCGAGCCGCACGTCGTCGTCGACGAACATCAGATGGTGGTGCGGCCAGCGGGCGAGCATCGCGTTGCGGGAGGCCGACAGG
     < A A A D L R V D D D V F M L H H H P W R A L M A N R S A S L
12787 CCATTGGTGGCACCGAGGATGCGCATGGTGCCGCCGGCGGCCCGGACCTCCTCGGCGACCTCCTCCGCCTCGGCCGTGACGGGCCGGTCCAG
     <G N T A G L I R M T G G A A R V E E A V E E A E A T V P R D L
12879 CAGGACGTAGTACTCGTCGCCGGAGAGCTGGGCCATGTTGTGCGCGAGGTGTTTCCTGACGTTCTCCACCCGGAACGCGCAGATCGCCACCA
     < L V Y Y E D G S L Q A M N H A L H K R V N E V R F A C I A V V
12971 CCATCGGGTGGTCGGACGGATCGCGGCTGACCACAGAGGCGTTGTTCGGCATCGTCCCTCGACATGAGCGTTGTGGGGCCGGCGGGGAGA
     < M P H D S P D R S V V S A N N P M
13061 GGCGGCCCACCGGATCGCGCTCCGCGGCAGCGTGCCGCGGCCCCGGCCGCCCCACGGACAGGTGGCGCACCGCAGCGCGGCGGGCCGTCCGG
13153 TGAGCGGCCGGGGGCGGAGCTCAGGCCGCTTCGTCCTTGCTGACGGTCGGCGGCCAGGTGCCCGCCGCGAGGATGCCCATCGCGTACGCCTT
13245 CGCGATCAGGGCCGGCCGGTTGGGCACTCGCAGGTTCTGCAACAGCTTGCTGACGTGGTACTCGACGCCCTGACGGCTGAGGTAGACCTTGT
13337 TGGCGATATGCACCGTCCGTTCGCCTGCGGCGATGCTTTCGATGATGCGCGCGTCCAGATCGGACAGTGAGAACTTGAGATTCACAACGCCC
13429 CCTTGATTGTGGATCTGTTGGCTCGTACGCGGCCAGACGTCATCGCCCGGACACCCCCCTGAGGTGCCGGTGGACGAGTGGTCGCTTCCGCT
13521 GGAAGACCGTCAGCGGCGGAAGGCCGGGTGCCCGCCACTCGTCGTCCTGCGCTTGCGGAGCTGTCTCAGTGTGCGGCGATGCCCCCGGCACG
13613 TAGCCCGCCTGACGGGCCTGTCGGCTTGGGCTCCAACTTCGGCAACCCATCGGTTCGCGCTGCACAGAACCAGCGGAGGAACATTGAGTTTC
13705 GAAGCCCTTCGCTACTGTCGATCGACATCACTGGCGAAATGAAACCGACCGGATTCGAGCCGATAGTTACGGAAAGTGACAATCGGCTGGCC
13797 CTGTCGCTCGCGCTGAACTCACCAATACGCCAAAAGCGTAGCCGGCCCACTGCGGAGCGTCCACCCCCCGAGGATATCGCCAGGCTTCCATG
13889 CAGAACTGGCAGGATCTTTCATCTCAGCCGCACCTGGCGACAAAACCCCTGCTCAAGACCATGAGTAAGCAGGCGCGGGAAATCCATGCAGT
13981 GACATGTGTCACTTTAGACAACCCAGCTCCAGCCAGGCCCACCACCCTGACAAAAGGGGCGGAATCGCGACCAGAGCGACACCAGCACATTC
14073 CTAGGGGATTCCTTAGTCTGGCGAGCGTCGATCCCCCACCCGTCAATCAATTGCCCGAACAAATTGCCCACCCGTCAAGATCAACCACTCCG
14165 CACCGTGAGCAGGCCGACCGTCCGGCAATGCGAACGACGACGTCCACCCCGTCCCGGTAGCCTCACCGCCGCTGGGGGGGCACGGGCCCGGA
14257 CACCGTCCGGCGTCGTGATCAGCGGGTCGCTCGCCGGCTGTCGCCCCGCGCGGGGACCGGCATCGCGCGCGGGGCCGGCACGAAGATCTCCG
14349 GCGACCTGTCAGCCCTGCAAGCGGACCGGCATCGCGCGCGGGGCCGGAACCACCCGACGGTTCAGCGCCGGGACCGATCGGGAAGCCGACT
                                                          < • R R S R D P L R S
14440 CGCGGCCTCGTCCCAGAGCCCGCCCACCGCATCCCGCAGCGATCGTCGGGGCCGCCACCCGAGCAGGTCACGCGCGGGCCCCGGGTCGACGC
     < A A E D W L G G V A D R L S R R P R W G L L D R A P G P D V R
14532 GGGCCCAGTCGACGACCTCCACCGAGCCGGGCCGATCCGGCAACTCCACCACCTCGGTCGGCACCCCGCTCACCTCGATCAACATCTCCACG
     < A W D V V E V S G P R D P L E V V E T P V G S V E I L M E V
14624 AGGGAGCGGACCGGAACGGCCTCCCCCCGCCCCACGCCGATCACCCGCCCGGTGACGGACTCCCGCGTGGCCGACACCACCGCCTCGGCGAC
     <L S R V P V A E G R G V G I V R G T V S E R T A S V V A E A V
14716 GTCCCGCACGTCGACGTAGTCCCGGTGGGCGCGCAACGGAGACAACTCCACCCTGGCCGACCGGTCGCGGCCCGCCGCGTCGACCAGGCGAA
     < D R V D V Y D R H A R L P S L E V R A S R D R G A A D V L R V
14808 CGACGACCCGCCCCAACAGGCTGTCGGGTGGCACGCCCGGACCCACCACGTTCGCGAGCCGCAGCACCGTCGCGTCCACCGAGCCGGCCCGC
     < V V R G L L S D P P V G P G V V N A L R L V T A D V S G A R
14900 GTCGCCGCGAGCACGGCCTGGGTGGCGGCCAGCTTCGCCCTGCCGTACATGCTCTCCGGCTGGGTGGGCACCGTGGCACCGGCGGGAGCCCC
     <T A A L V A Q T A A L K A R G Y M S E P Q T P V T A G A P A G
14992 GGGTGGCTCCTGGACGCGTTCCAGGACCGAGCCGAGGTGCACCAGCCTGGGCCGGCAACGGGTGCGCTCCAGCGCCGCGGTGACACTCCACG
     < P P E Q V R E L V S G L H V L R P R C R T R E L A A T V S W T
```

Figure 11D

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15084 TCGGGATCGTGCAGCTCGACGGCAGCTCGGCGTCCGTCAGGTTCCACTTGCCGCCGGTGGCGTTGACCACCGCGTCGGGCTGCTCGGCGTCG
      <  P  I  T  C  S  S  P  L  E  A  D  T  L  N  W  K  G  G  T  A  N  V  V  A  D  P  Q  E  A  D
15176 AACACGGCGGCCAGCGCGGCGGGCTCCAGGGTGGCGACGTCCAGCGCCCGGGCCCGGTACGGCAGCCCCGCCGACGGGACGCGGCGGGCCAA
      <F  V  A  A  L  A  A  P  E  L  T  A  V  D  L  A  R  A  R  Y  P  L  G  A  S  P  V  R  R  A  L
15268 CACGAGGACGTCGTCGCCCCGGGCGGCAAGCGCGGCGCTCACGTGACGCCCGACGAAGCCCGTACCACCGACGACCACGACACGCCGCGCGC
      <  V  L  V  D  D  G  R  A  A  L  A  A  S  V  H  R  G  V  F  G  T  G  G  V  V  V  V  R  R  A  G
15360 CCATCCGTACCTCCTGGGGATCAGTCTCGTGCGCCGGCGGCGTCCAGGCGACCGCCCGGCCCCTGACAGGTCACGGGGGCGCGCAACAC
      <  M                    <  •  D  R  A  G  A  A  D  L  R  G  G  P  G  Q  C  T  V  P  A  R  L  V
15449 CCTGGCCCGGTCGCGAACCTCGTCCAGCAGCCGGGCCCGGGCGCGGATCGCCGTCACCTCCTCCGCCGGCTGACCGGCGGTGACGGCGCGGA
      <  R  A  R  D  R  V  E  D  L  L  R  A  R  A  R  I  A  T  V  E  E  A  P  Q  G  A  T  V  A  R  V
15541 CGAACTCTCGCATCGTGTTGACGAACTGGTCCTCGGCCGGGAAGGTCAGCTCCCGCGTCTCGTCCTGCCGCTCCACCCGCACCACCGGGTGC
      <  F  E  R  M  T  N  V  F  Q  D  E  A  P  F  T  L  E  R  T  E  D  Q  R  E  V  R  V  V  P  H
15633 CAGGCCGGCGGTGGGGTGTACGCCCGGTCGACGACGATCCGGCCGGCGCTTCCCCAGAGCTGGTACTCGCACCGGTAGGAGTGCTCGAAACC
      <W  A  P  P  P  T  Y  A  R  D  V  V  I  R  G  A  S  G  W  L  Q  Y  E  C  R  Y  S  H  E  F  G
15725 GAAGGCGATCTGTGCGGTCCGCCCGTCCGGCGTACACAACAGCGCGGCACCCGAAACGTCCACGCCGCGATCGGGGTCCTCCCGGAGGGTGG
      <  F  A  I  Q  A  T  R  G  D  P  T  C  L  L  A  A  G  S  V  D  V  G  R  D  P  D  E  R  L  T  A
15817 CCGCCACCACCTCCGGCTCCTCCGGCAGGAAGAACCGGGCCGCGCCCAACGGGTAGACGCCCAGATCCAGCAGCGCTCCGCCACCCAGCTCG
      <  A  V  V  E  P  E  E  P  L  F  F  R  A  A  G  L  P  Y  V  G  L  D  L  L  A  G  G  G  L  E
15909 GGTCGGTAACGGATGTCGCCCGCAGGCAGCGGCGGAAACCCGAAGACGCCGGAGACCATCCGCAGCTCGCCGATCTCGCCGGCCGCGACCAT
      <P  R  Y  R  I  D  G  A  P  L  P  P  F  G  F  V  G  S  V  M  R  L  E  G  I  E  G  A  A  V  M
16001 CCGGCGCACGAAGTGGTGCACCCCATGTCGGAGGAAGGTGAGGTTGTCCATCAACACGAGCCCACGCGACCGGGCCTGGGTCAGCACCGCCG
      <  R  R  V  F  H  H  V  G  H  R  L  F  T  L  N  D  M  L  V  L  G  R  S  R  A  Q  T  L  V  A  A
16093 CGGTGTCGACCAGCCGGGTGGTCAGCGGCTTCTCCACCAGCACGTGTTTGCCCGCGGCCAGGGCGCGTTCGATCCAGGTGTGGTGCAGCCCG
      <  T  D  V  L  R  T  T  L  P  K  E  V  L  V  H  K  G  A  A  L  A  R  E  I  W  T  H  H  L  G
16185 GTCGGCAGCGGAATGTAGACGGCATCGATGTCCGGGCGGTCGAGAACGGACTGGTAGCCCTCGGCGGCGGCGCACCCGAACTCCGCGGCGAA
      <T  P  L  P  I  Y  V  A  D  I  D  P  R  D  L  V  S  Q  Y  G  E  A  A  A  C  G  F  E  A  A  F
16277 GGCGCGCGCCTTGGCCAGTTCCCGCGCGACCACCACGAGCTCCGCCTCCGGGACCCGCCTGATCGCCGGCAGGGCACGGCGGCGCGCGA
      <  A  R  A  K  A  L  E  R  A  A  V  V  V  L  E  A  E  P  V  R  R  I  A  P  L  A  R  R  R  A  I
16369 TGTCGGCGCAGCCGAGAACCCCGATGCGGACCGTCATCTCCGCCATCGGGTCACCACAGGCTGCGCAGGCAGGCCAGCAAGCTGCGGGCC
      <  D  A  C  G  L  V  G  I  R  V  T  M  E  A  M     <  •  W  L  S  R  L  C  A  L  L  S  R  A
16459 TCGATGTTGAGGTAGTAGCCGTGCCGGAGCAGGGCCTCCAGCTGGCGCACCGTCACCCAGCAGAACTCGTCCGGCACCTCGGTCGGGAAGTC
      <E  I  N  L  Y  Y  G  H  R  L  L  A  E  L  Q  R  V  T  V  W  C  F  E  D  P  V  E  T  P  F  D
16551 GTCGCCGGCGTCGACCAGGAGGTAACGGTTCTCCGACCGGTAGAATCGCCCGCCCTCCTCGGTGAGCACGGTGTCGTAGAGGACACGCTCGG
      <  D  G  A  D  V  L  L  Y  R  N  E  S  R  Y  F  R  G  G  E  E  T  L  V  T  D  Y  L  V  R  E  P
16643 GGGCGGCTTCCAGCACCTCGGCCAGGAACAGTGGTCGGGGGCCGGGCTGGTTGTCCGGGATGCACTGCACCGTTGGGCCCATCTCCATCGCG
      <  A  A  E  L  V  E  A  L  F  L  P  R  P  G  P  .Q  N  D  P  I  C  Q  V  T  P  G  M  E  M  A
16735 TCGAGCAGCCCCGCCTGGTAGCGCGCGTGCACCAGCAGGTGCGCCACTCCGTCGATTTCCTTGACCAGGAAGGCGACCACGCCCCGGTGCCG
      <D  L  L  G  A  Q  Y  R  A  H  V  L  L  H  A  V  G  D  I  E  K  V  L  F  A  V  V  G  R  H  R
16827 CGGATACAACAGCGGCTGACTCCACCCGGTCACCTCGCGGTTGTCGATGCGCACCGTGACGCCGACCACGGAGAAGTGCCGGCCGTCGTCCC
      <  P  Y  L  L  P  Q  S  W  G  T  V  E  R  N  D  I  R  V  T  V  G  V  V  S  F  H  R  G  D  D  R
16919 GCGCGATCCCGTCCGCGGTGTGCCGCCAGTCCGGCAGCCCTCGTAGCGGCACCCGCCGCACGGTCATCTCGTGCCGGCCCTTGGCCCCGGTG
      <  A  I  G  D  A  T  H  R  W  D  P  L  G  R  L  P  V  R  R  V  T  M  E  H  R  G  K  A  G  T
17011 AACCAGCTCAACACCGACACCAGGTCGTGGCGGCCGGGGGCGCCCGCCGCCGAGCGCACGATCGCCGCCACCGCCGGCGACGACGGCGCCTC
      <F  W  S  L  V  S  V  L  D  H  R  G  P  A  G  A  A  S  R  V  I  A  A  V  A  P  S  S  P  A  E
17103 GGTCTCCTGGGCCGCGGCGTAGAAGGCCGAGGGCAGACATGACAGCACCGTACGCGTGTCCATGTTGACCAGGCCGTCCACCCGCAGCAGCG
      <  T  E  Q  A  A  A  Y  F  A  S  P  L  C  S  L  V  T  R  T  D  M  N  V  L  G  D  V  R  L  L  A
17195 CGAGCAGTTCGCGCAGCGGGAGCCACCGGTGGTAGTCGCCGGCCGGCACGTCCTCGTCGACCTGGACCACCATGTTCCGGTTGCGCTTGCGC
      <  L  L  E  R  L  P  L  W  R  H  Y  D  G  A  P  V  D  E  D  V  Q  V  V  M  N  R  N  R  K  R
17287 AGGAACCAGGAGCCCTGCTCCGACTGCAGGACGTCAACCAGCACCCGACCGGCCCCCGGGCGGGTGAAGTAGTCGAGGTACTTCGTGCCGCC
      <L  F  W  S  G  Q  E  S  Q  L  V  D  V  L  V  R  G  A  G  P  R  T  F  Y  D  L  Y  K  T  G  G
17379 GCCACGGTGCACCCGGGTGTAGTTGCTCCGGGTGGCCTGCACCGTCGGCGAGAGCTGCATGACGTTGATGTTGCCGGGCTCCACCTTGGCCT
      <  G  R  H  V  R  T  Y  N  S  R  T  A  Q  V  T  P  S  L  Q  M  V  N  I  N  G  P  E  V  K  A  Q
17471 GGAGCAGGCAGTACGGTGTCCCGTCGACGACCTTGACGAGCATGCCGAGGATGCCGATCTCCGGCTGGTTGATGATCGGCTGGTGCCATTCG
      <  L  L  C  Y  P  T  G  D  V  V  K  V  L  M  G  L  I  G  I  E  P  Q  N  I  I  P  Q  H  W  E
17563 CGCACCGCGCCGTAGGTGGTCTGGACGTGCAGCCCCTCGATCACGAAGAACCGGCCGCTCTCGTGCCCGAGGTTGCCGGTCACCGGGTCGAA
      <R  V  A  G  Y  T  T  Q  V  H  L  G  E  I  V  F  F  R  G  S  E  H  G  L  N  G  T  V  P  D  F
17655 CGCCCACCCGGGCAGCCGGTCCAGCGGCACGCGGTCCACCCGGCAGTAGGTCGACCGGGTCCGCTCGGCGAACCAGGAGAGGAAGTCCGGCC
      <  A  W  G  P  L  R  D  L  P  V  R  D  V  R  C  Y  T  S  R  T  R  E  A  F  W  S  L  F  D  P  R
17747 GGACCCCCTCGGCGTGCAACGCCGACCACGAGCCGCCGTCGACCGGGCCGGGCCGGTGCGGGCCCGCGTCCCGGGTCAGCAACGGCCCGTCG
      <  V  G  E  A  H  L  A  S  W  S  G  G  D  V  P  G  P  R  H  P  G  A  D  R  T  L  L  P  G  D
17839 GCGCGGACCTTCGGGTCGGGCGACGAATCGCTCACCACAGCTCGGCCAGTTCGGCGGAAAAGGCGTGGGAAGACCCGTCCGTGTCCGCCAA
      <A  R  V  K  P  D  P  S  S  D  S  V
                                          <  •  W  L  E  A  L  E  A  S  F  A  H  S  S  G  D  T  D  A  L
17930 CAGGCGCAGATCGCTGTCGACCATCATGGCGACCATCTCCTCGAAGGAGACGGAGGGTTTCCAGCCGAGCCGCTGGCGGGCCTTCGTCGGAT
      <  L  R  L  D  S  D  V  M  M  A  V  M  E  E  F  S  V  S  P  K  W  G  L  R  Q  R  A  K  T  P  D
18022 CCGCGCAGAGCAGCTCGACCTCGGCGGGCCGGATGAGCGACTCGTCCACCACCACGTGGTCCCGCCAGTTGAGGCCCACGTGGGCGAAGGCC
      <  A  C  L  L  E  V  E  A  P  R  I  L  S  E  D  V  V  V  H  D  R  W  N  L  G  V  H  A  F  A
18114 GCCTCGACCAGCTCGCGGACGCTGTGCGTGACCCCCGTGCCGAGGACGTAGTCCTCCGGCTCGTCCTGGGCCAGCATCAGGACCATGCCCCG
      <A  E  V  L  E  R  V  S  H  T  V  G  T  G  L  V  Y  D  E  P  E  D  Q  A  L  M  L  V  M  G  R
18206 CACGTAGTCGCCCGCGAAGCCCCAGTCCCGCTCGGCCGAGAGGTTGCCCAGGCGAAGCGAGCTGCGAATGCCCAGCTTCACCGCCGCCACGC
      <  V  Y  D  G  A  F  G  W  D  R  E  A  S  L  N  G  L  R  L  S  S  R  I  G  L  K  V  A  A  V  G
18298 CCAGCGACACCTTGCGGGTGACGAACTCGGGACCACGCACCGGTGATTCGTGGTTGAACAGAATGCCGGAGACGGCATACATGCCGTACGAC
      <  L  S  V  K  R  T  V  F  E  P  G  R  V  P  S  E  H  N  F  L  I  G  S  V  A  Y  M  G  Y  S
18390 TCACGGTAGTTCTGCACCATGTAATGCCCGAACGCCTTGGCCGCGCCGTACGGGCTACGCGGATGGAACGGGGTCAGCTCATTCTGGACGGG
      <E  R  Y  N  Q  V  M  Y  H  G  F  A  K  A  A  G  Y  P  S  R  P  H  F  P  T  L  E  N  Q  V  P
18482 CTCCCGCACCTTGCCGAACATCTCCGACGAAGACGCCTGATAAAAGCGCGGCTGACCGGCTGCGGGACTGCGGGAATCCGACAGGCCCCCCA
      <  E  R  V  K  G  F  M  E  S  S  S  A  Q  Y  F  R  P  Q  G  A  A  P  S  R  S  D  S  L  G  G  V
18574 CGATCCGCAAGGCTTCGAGCATGCGGAGCACACCCATGCCGGTGACCTCCGCCGTCGTGGTGGACTGCCGCCACGACACCGGCACGTACGAC
      <  I  R  L  A  E  L  M  R  L  V  G  M  G  T  V  E  A  T  T  T  S  Q  R  W  S  V  P  V  Y  S
```

Figure 11E

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18666 AGCGCGCCGAGGTTGTAGACCTCGTCCGGCGCCGCGCGTTCGATCGCCGCCACCAGGCTCGTCTGATCCAGAAGGTCGCCGCTGATCAGCTT
     <L  A  G  L  N  Y  V  E  D  P  A  A  R  E  I  A  A  V  L  S  T  Q  D  L  L  D  G  S  I  L  K
18758 GACCGCTGGATCAGGTTGCCGAAGGCTGCGGACCGAGGGCGCGGTCTGCCCGCGCACCAATCCAAATACCTCGTATCCGGACTGAAGCAGGT
     <  V  A  P  D  P  Q  R  L  S  R  V  S  P  A  T  Q  G  R  V  L  G  F  V  E  Y  G  S  Q  L  L  H
18850 GCTCCGCGAGATACGTGCCGTCCTGGCCGGTAATTCCAGTGATCAGCGCCCGCCGTGTCAGGGTAGTCTCCAGCCGTGAAGCCACCTGGCC
     <  E  A  L  Y  T  G  D  Q  G  T  I  G  T  I  L  A  R  R  T  L  T  T  E  L  R  S  A  V
18941 GAGGCGTGACCTCGCGCCGATGGCGGACCAAAGATCCGCCCGTTCGAAATGGGGTCGGATCTCCCGCTACCGCGCTCACGGTACGCGAATCT
19033 CCAAGCGGATTCAGCGACCCGGAAAGCAATATAGGGAGGTTACTAGTAGTACTTTCCGGCGGGCCGGCAGCGACGCCCGGCCCGGACCGGCA
19125 GGATCGCCCCGTTCGGCCGGCGGACCCATCCCGGACACCTTCCACCGAAGCTCTTCGGGATCGTCGCCCGCCGATGCGAACTGCTTGACTCC
19217 ACCGTTTTGTCCCCCTAACGTCGGCGAGGCTGCCAGCCGGCCCGCGAGCCGGGCCGGGTTCACGAAGGCGCCAACTTCCGGTGAGAGAGCAG
19309 GGCTCATGTCGCAGAGCCGGCCCGCGGCCGCAGCACCCCCAGCCCGCCTGCCACGTCGCCGCGCCATGGTCGCGTTGGTCGCGGTGATGAT
                                                                    >  M  V  A  L  V  A  V  M  I
19400 CCCGATGGTGCTGGCCACCCTCGACAACACCATCATCGGCACCGCACTGCCCACCGTGGTCGGCGAGTTGGGCGGCCTCAGCACGCTCTCCT
     >  P  M  V  L  A  T  L  D  N  T  I  I  G  T  A  L  P  T  V  V  G  E  L  G  G  L  S  T  L  S
19492 GGGTGATCACCTCGTACACGCTGGCCACGGCCGCCTCCACGCCGGTCTGGGGCAAGCTCGCCGACATGTACGGCGGCAAGGTGGTCTTCGTG
     >W  V  I  T  S  Y  T  L  A  T  A  A  S  T  P  V  W  G  K  L  A  D  M  Y  G  G  K  V  V  F  V
19584 GCCACGCTGGTCGTGTTCCTGGCCGGGTCGCTGCTGTCCGGCATGGCGCAGAGCATCACCCAGCTGACCGTCTTCCGGGCCGTGCACGGGCT
     >  A  T  L  V  V  F  L  A  G  S  L  L  S  G  M  A  Q  S  I  T  Q  L  T  V  F  R  A  V  H  G  L
19676 CGGCGCGGGCGGCCTGATGGTCTGCGCGTTCGCCATCATGGTGGAGGTTCTCGCCGGCCCTGACCTGCCCAAGTACCAGGGCATCATGTCGG
     >  G  A  G  G  L  M  V  C  A  F  A  I  M  V  E  V  L  A  G  P  D  L  P  K  Y  Q  G  I  M  S
19768 CGACCATGGGCCTGACCATGGTGGCGGGCCCGCTCGTCGGCGGCCTGATCACCGATGAGCTCGGCTGGCGCTGGTGCTTCTACATCAACCTG
     >A  T  M  G  L  T  M  V  A  G  P  L  V  G  G  L  I  T  D  E  L  G  W  R  W  C  F  Y  I  N  L
19860 CCGATCGGGGCGGTCGCGCTGCTCATCGTGGTGCTGATGATGCACCTGCCGCGCCGACACACCAAGGCCCGGATCGATTACGCGGGTGCTGC
     >  P  I  G  A  V  A  L  L  I  V  V  L  M  M  H  L  P  R  R  H  T  K  A  R  I  D  Y  A  G  A  A
19952 CCTGCTCACCGTGGTCAGTTCGTGCGTCGTGCTGGTGACCACCTGGGGCGGCATCACCTACCCCTGGGCGTCTCCGATGATCCTGGGGCTGG
     >  L  L  T  V  V  S  S  C  V  V  L  V  T  T  W  G  G  I  T  Y  P  W  A  S  P  M  I  L  G  L
20044 TCGCGCTCGGGGTGCTGACCTGCGCGCTCTTCGTGGTGGTCGAGCGACGGGTGGCCGAGCCGTTGGTGCCCCTGGCCATGTTCCGCAGCCTG
     >V  A  L  G  V  L  T  C  A  L  F  V  V  V  E  R  R  V  A  E  P  L  V  P  L  A  M  F  R  S  L
20136 AACTTCACCCTGAGCACCCTCATCGCCTTCCTGGTCGGCTTCGCCCTCATCGCGGGGCTGACCTTCCTGGCCCTGTTCCAGCAGGCGGTGCA
     >  N  F  T  L  S  T  L  I  A  F  L  V  G  F  A  L  I  A  G  L  T  F  L  A  L  F  Q  Q  A  V  Q
20228 GGGTGCCTCCGCGTCCGACTCCGGCCTGTTGCTGCTGCCCCTGCTGCTGTCCATGGCGGCGGTCAACGTGGTCGGGGGTCGCCTGATGAGCG
     >  G  A  S  A  S  D  S  G  L  L  L  L  P  L  L  L  S  M  A  A  V  N  V  V  G  G  R  L  M  S
20320 GCGGGCGTTCCTACCGGCTGCTGATGCTCGCCGGTGCGGCGCTGATGACCCTGAGCCTGCTGCTCTTCGCCCTGATGGACGTGGGCACCAGC
     >G  G  R  S  Y  R  L  L  M  L  A  G  A  A  L  M  T  L  S  L  L  L  F  A  L  M  D  V  G  T  S
20412 CGGACGGTCACCGCGATCCCCATGGTCGGCTTCGGCGCAGGGCTGGGGCTGCTCATGCAGACCAGCCTGATGGTGGCGCTGAGCAGCGTGGA
     >  R  T  V  T  A  I  P  M  V  G  F  G  A  G  L  G  L  L  M  Q  T  S  L  M  V  A  L  S  S  V  E
20504 GATGAGGAACCTCGGGGTGGCCGCCTCCACGTCCACGCTCTTCCGCACCATCGGTGGGGCGGTGGGGGCGTCGGCGACGGTCTCGCTGTTCT
     >  M  R  N  L  G  V  A  A  S  T  S  T  L  F  R  T  I  G  G  A  V  G  A  S  A  T  V  S  L  F
20596 CCGTGCGGGTGCAGTCGGCGCTGGCCGATCGGGGGGTCGCCGACGTGGCTGACCTCCTCGGCCACTCCGCGCGGCTGGACGCCGCCGGGCTG
     >S  V  R  V  Q  S  A  L  A  D  R  G  V  A  D  V  A  D  L  L  G  H  S  A  R  L  D  A  A  G  L
20688 GCCCAACTCCCCCGGGCCGTCCGTGTCCACTTCATGCACGCGGTGGCCTCCGGCACCCGGTGGGCCTTCCTGATGACCGTGCTGGCGGGGCT
     >  A  Q  L  P  R  A  V  R  V  H  F  M  H  A  V  A  S  G  T  R  W  A  F  L  M  T  V  L  A  G  L
20780 GATCTGCGTCGCGGCGGCGTGGTTCCTGCGCCGGGTCACCCCGTTGACGTCGGCACCGGTGGCACCCGAACCGGCGCGCGACGTCGCCGCGC
     >  I  C  V  A  A  A  W  F  L  R  R  V  T  P  L  T  S  A  P  V  A  P  E  P  A  R  D  V  A  A
20872 CCGCCGCCAGCAGCGGGCGCGCGCCGAACTACTAGCGGATTTCCTAGGGTTCCTCGTCGACGGTAGAGCTGAATTCACCGGCGACCTAACA
     >P  A  A  S  S  G  R  A  P  N  Y  •
20963 TTCTTTTCGCGATCCGGAATCCGTCCATTCCCCTGTCTGGCGATGGTCGACGGGCCGGCCCGTGCCGAGCGGACAGACACAGATTCTCGGAT
21055 TGGAGCTCGATGTCCAGCAAGATCCTAGTCATCGGTGGAGGTCCGGCCGGATCCACGGCCGCCGCGCTGCTCGCCCGATCGGGGCTGTCG
                 >M  S  S  K  I  L  V  I  G  G  G  P  A  G  S  T  A  A  A  L  L  A  R  S  G  L  S
21145 GTGACGCTCCTGGAAAAGGAGACGTTCCCGCGATACCACATCGGCGAGTCGATCGCGTCCTCGTGCCGCACCATCGTCGATTTCGTGGGCGC
     >  V  T  L  L  E  K  E  T  F  P  R  Y  H  I  G  E  S  I  A  S  S  C  R  T  I  V  D  F  V  G  A
21237 TCTCGACGAGGTCGACTCGCGGGGCTACCCGCAGAAGAACGGGGTCCTGCTGCGCTGGGGCAACGAGGACTGGGCCATCGACTGGGCCAAGA
     >  L  D  E  V  D  S  R  G  Y  P  Q  K  N  G  V  L  L  R  W  G  N  E  D  W  A  I  D  W  A  K
21329 TCTTCGGTCCGGGCGTGCGGTCCTGGCAGGTCGACCGGGACGACTTCGACCACGTCCTGCTCAACAACGCCGGCAAGCAGGGCGCCAAGATC
     >I  F  G  P  G  V  R  S  W  Q  V  D  R  D  D  F  D  H  V  L  L  N  N  A  G  K  Q  G  A  K  I
21421 ATCCAGGGCGCGGCTGTCAAGCGGGTGTTGTTCGACGGTGAGCGGGCCACCGCCGCCGAGTGGTTCGACCCCGAGTCGGGTGAGGTCCGCAC
     >  I  Q  G  A  A  V  K  R  V  L  F  D  G  E  R  A  T  A  A  E  W  F  D  P  E  S  G  E  V  R  T
21513 CATCGATTTCGACTACGTGGTCGACGCGTCCGGCCGGGCCGGGCTGATCCCGTCCCAGCACTTCAAGCACCGGCGCCCCACCGAGACGTTCA
     >  I  D  F  D  Y  V  V  D  A  S  G  R  A  G  L  I  P  S  Q  H  F  K  H  R  R  P  T  E  T  F
21605 AGAACGTGGCCATCTGGGGCTACTGGCAGGGTGGCTCGCTGCTGCCGAACTCTCCCTCCGGCGGGATCAACGTCATCTCCGCGCCCGACGGC
     >K  N  V  A  I  W  G  Y  W  Q  G  G  S  L  L  P  N  S  P  S  G  G  I  N  V  I  S  A  P  D  G
21697 TGGTACTGGGTCATTCCGCTGCGCGGCGACCGGTACAGCATCGGCTTCGTCTGCCACCAGAGCCGCTTCCTGGAGCGGCGCAAGGAGCACGC
     >  W  Y  W  V  I  P  L  R  G  D  R  Y  S  I  G  F  V  C  H  Q  S  R  F  L  E  R  R  K  E  H  A
21789 CTCGCTGGAGGACATGCTCGCCGCACTGGTACAGGAGTCCCCGACCGTGCGCGGCCTGACGGCGAACGGGACGTACCAGCCGGGCGTGCGGG
     >  S  L  E  D  M  L  A  A  L  V  Q  E  S  P  T  V  R  G  L  T  A  N  G  T  Y  Q  P  G  V  R
21881 TGGAGCAGGACTTCTCGTACATCTCCGACAGCTTCTGCGGGCCCGGCTACTTCGCGGCCGGCGACTCCGCCTGCTTCCTGGACCCACTGCTG
     >V  E  Q  D  F  S  Y  I  S  D  S  F  C  G  P  G  Y  F  A  A  G  D  S  A  C  F  L  D  P  L  L
21973 TCCACCGGCGTGCACCTCGCCCTCTACAGCGGCATGCTCGCCTCGGCGTCCATCCTGGCCACCATCCACGGTGACGTCACCGAGGAGGAGGC
     >  S  T  G  V  H  L  A  L  Y  S  G  M  L  A  S  A  S  I  L  A  T  I  H  G  D  V  T  E  E  E  A
22065 GCGGGCGTTCTACGAGTCCCTCTACCGCAACGCCTACCAGCGCCTGTTCACCCTCGTCGCCGGCGTCTACCAGCAGCAGGCCGGCAAGAGGG
     >  R  A  F  Y  E  S  L  Y  R  N  A  Y  Q  R  L  F  T  L  V  A  G  V  Y  Q  Q  Q  A  G  K  R
22157 CATACTTCGGCCTGGCCGACGCGCTGGTGCACGACAGCGGCGAACCCGAGTACGAGAAGGTAGACGGGGCCCGCGCCTTCGCCCAGCTCGTC
     >A  Y  F  G  L  A  D  A  L  V  H  D  S  G  E  P  E  Y  E  K  V  D  G  A  R  A  F  A  Q  L  V
22249 GCCGGCCTCGCCGACCTGGACGACGCGGCGGAGGGACGGCACGACAGCACCGCGGCGGCGGCACCGGCGGAGCAGGACAACTCCGTCCGGCA
     >  A  G  L  A  D  L  D  D  A  A  E  G  R  H  D  S  T  A  A  A  A  P  A  E  Q  D  N  S  V  R  Q
22341 GCTCTTCCTGGCCGCCGAGGAGGCCCGCCGGATGGCCGACGCGCGCACGCCGAGCGCCCCGGTCAGCGAGGCGCCGGGCAAGCTCGACAGCC
     >  L  F  L  A  A  E  E  A  R  R  M  A  D  A  R  T  P  S  A  P  V  S  E  A  P  G  K  L  D  S
22433 ACGACCTCTTCGACTCGGCAACCGGCCTCTACCTGGTCACCACCCCGCGACTGGGGATCCGCCGGGCCAAGCCGGCCGACACGCAGGCGGCG
     >H  D  L  F  D  S  A  T  G  L  Y  L  V  T  T  P  R  L  G  I  R  R  A  K  P  A  D  T  Q  A  A
```

Figure 11F

```
22525 GCAGAGCAGTCTGCCTGAGGTTCCACCCCTGGTGGCCCCCGGCCCGGACCGCGCCGGTCCGGGGGCTGCTCAACCCTCCCACCAACATCCG
      > A  E  Q  S  A  •
22616 GCATCCGGTGCCGGCGGCTGAGCAGGGGCAGCGCCACCGACTCCGGCCCGTCACATGGACAAGGTCACCTCTCCCGTGCTGAACAGACGACA
22708 GTTGCTCGCCCTCGGCAGCGTGGCCGCCGGAGGCACCGTCATGTCACGCTCCCTCAGACGGGACGCGCAGGCCGCCCAGGCGGCACCGGC
                                                  > M  S  R  S  L  R  R  D  A  Q  A  A  Q  A  A  P  A
22798 GTCGCCCGCCAACCCGCACGCCGGGCACGCCGCCCCGGTGCCCAGCCGGGTCAGCACGACCACGGTCGCGGTCACCCCGTTCACCGAGCCGA
      > S  P  A  N  P  H  A  G  H  A  A  P  V  P  S  R  V  S  T  T  T  V  A  V  T  P  F  T  E  P
22890 TGCCCGTCCCGCCGCGGCTGACCCCGGTCTCCCGCCGCGACGGCATCGACGTCTACGAGATCCCCATCCGGCCGGCGCAGGTGCAGATCCTG
      >M  P  V  P  P  R  L  T  P  V  S  R  R  D  G  I  D  V  Y  E  I  P  I  R  P  A  Q  V  Q  I  L
22982 CCCGGCCTGCTCACGCCCGCCTACACCTACGCCGGTTCCTTCGTCGGCCCCACCATCCGGGCCCGCACGGGCCGGCCCGTGCGGATCACCTA
      > P  G  L  L  T  P  A  Y  T  Y  A  G  S  F  V  G  P  T  I  R  A  R  T  G  R  P  V  R  I  T  Y
23074 CACCAACGGGCTCGACACCCACGCCAACGTGCACCTGCACGGCGGGCACGTGCCGGCCACCAGCGACGGTCACCCGATGGACCTGATCCCGC
      > T  N  G  L  D  T  H  A  N  V  H  L  H  G  G  H  V  P  A  T  S  D  G  H  P  M  D  L  I  P
23166 CGGGCGGCTCGAAGGTCTACGACTACCCGAACCTTCAGCGCGGCGCGACGCTCTGGTACCACGACCACACCCACGCCTACGAGGCCGACCAC
      >P  G  G  S  K  V  Y  D  Y  P  N  L  Q  R  G  A  T  L  W  Y  H  D  H  T  H  A  Y  E  A  D  H
23258 GTCTACCGCGGACTGCACGGCTTCTATCTGATCGACGACCCGGCCGAGCATCACCTGCGCCTGCCCGCCGGCAAGTACGACGTGCCGATCAT
      > V  Y  R  G  L  H  G  F  Y  L  I  D  D  P  A  E  H  H  L  R  L  P  A  G  K  Y  D  V  P  I  M
23350 GCTGCGCAACGCCCAGTTCGACGACTCCGGCGCCCTCGTCTTCGGCCACCCGGACGACCGGGTCACCATCCTGGCGAACGGCAAGGCCCAGC
      > L  R  N  A  Q  F  D  D  S  G  A  L  V  F  G  H  P  D  D  R  V  T  I  L  A  N  G  K  A  Q
23442 CCTACTTCGAGGTGGCCCCGCGCAGGTACCGGTTCCGCCTGCTCAACGCGGCGCTGAAGCACGTCTTCCGGCTCAACCTGGGCGGCGAACCG
      >P  Y  F  E  V  A  P  R  R  Y  R  F  R  L  L  N  A  A  L  K  H  V  F  R  L  N  L  G  G  E  P
23534 CTCACCCGCATCGCCACGGACGGCGGGCTGCTGCCCGCCCCCACCAGTCACACCGAGCTGGCGCTCTCCTCCGGGGAGCGGGTCGAGATTGT
      > L  T  R  I  A  T  D  G  G  L  L  P  A  P  T  S  H  T  E  L  A  L  S  S  G  E  R  V  E  I  V
23626 GATCGACTTCGCCGAGCACGCAGGCGGCGGGCCGGTCTACCTCTACGACGGGGACAACCCGATCCTGCGCTTCGACGTGTCGTCCCGGGCGG
      > I  D  F  A  E  H  A  G  G  G  P  V  Y  L  Y  D  G  D  N  P  I  L  R  F  D  V  S  S  R  A
23718 TCACCGACCCCAGCCGGGTGCCGGTCACCCTGCGCGCACTGCCCCCGATGGGCACGCCGACCGTGGAGCGCACCGTGTCGATGAGCTTCGAC
      >V  T  D  P  S  R  V  P  V  T  L  R  A  L  P  P  M  G  T  P  T  V  E  R  T  V  S  M  S  F  D
23810 ATGTCGGCCCGGCCCCCGATCGCGCTCATGGACGGCAAACCGTTCGACCCTCTCCGGGTGGACGTACAGGTCAAGCGGGGCAGCACCGAGAT
      > M  S  A  R  P  P  I  A  L  M  D  G  K  P  F  D  P  L  R  V  D  V  Q  V  K  R  G  S  T  E  I
23902 CTGGAACGTGGTCAACGCGGATACCGATCCGTTCCCCTTCGACCATCCGTTCCACCTGCACCTGGTGACGTTCCGGGTGCTCGGCCGCGACG
      > W  N  V  V  N  A  D  T  D  P  F  P  P  F  D  H  P  F  H  L  H  L  V  T  F  R  V  L  G  R  D
23994 GCGGGCCGCCCGCCGCGGAGGACGCCGGGCTCAAGGACACCGTCTACGTCTCGCCCAAGGGGTCTGTCAAGATCCAGGTCACCTTCGCCACG
      >G  G  P  P  A  P  E  D  A  G  L  K  D  T  V  Y  V  S  P  K  G  S  V  K  I  Q  V  T  F  A  T
24086 CCGTACCTCGGGCAGTACGTCTACCACTGCCACTACCTGGAGCACTCGTCGCTGGGGATGATGGCCCAGCTGGAGGTTGTGCCCTGAGGGC
      > P  Y  L  G  Q  Y  V  Y  H  C  H  Y  L  E  H  S  S  L  G  M  M  A  Q  L  E  V  V  P  •
24177 TCAGCCGTGCAGGTCGACGATCGAGGGGTGGGCGCCGAACAGGCTGACCGGCCGCACGTCGCCCACCCCGAACCCGGCGGCGCGGGCCAGG
      < •  G  H  L  D  V  I  S  P  H  A  G  F  L  S  V  P  R  V  D  G  V  G  F  G  A  A  R  A  L
24268 TCGGCCTGGTCGGCGAACTCGTGCAGCAGCAGTACCGCCCGCCCGCCGTCGACCGTCACCCGGCGCAGCTCCGCGAAGAGGCGGCCGGAATC
      <D  A  Q  D  A  F  E  H  L  L  L  V  A  R  G  G  D  V  T  V  R  R  L  E  A  F  L  R  G  S  D
24360 ACCGGCGAGCACGCCCCGCGCCTGCACCTGCCGGTCCCAGGGCGGATTGCTGACCACCCGGTCCACCCGACCGGTCCGCAGCGGCAATCGTC
      < G  A  L  V  G  R  A  Q  V  Q  R  D  W  P  P  N  S  V  V  R  D  V  R  G  T  R  L  P  L  R  G
24452 CGGCGTCGGCGACCGCCCAGGTGACGCGGGCCCCCGACGCCGCCGAGTTGGCGACGGCCGCGCCGACCGTCTCCGGGTCGTGGTCCGAGCCG
      < A  D  A  V  A  W  T  V  R  A  G  S  A  A  S  N  A  V  A  A  G  V  T  E  P  D  H  D  S  G
24544 AACAGCACCGCCCCCGGTGCCAGCCCGGCTGCCTCCACGGGGATCGTGCCGGTGCCGCAGCACGGATCGGCCACCAGCATCCCGGGGCGGAT
      <F  L  V  A  G  P  A  L  G  A  A  E  V  P  I  T  G  T  G  C  C  P  D  A  V  L  M  G  P  R  I
24636 GCCGGCCAGCCAGGCCAGCGCCGCGGCGAGCGGCGGATGCAGGGTCCCCGGCGTGGACGACCGCTTGTAGGCCCGCCGGTGCAGCGGCCGGT
      < G  A  L  W  A  L  A  A  A  L  P  P  H  L  T  G  P  T  S  S  R  K  Y  A  R  R  H  L  P  R  D
24728 CGGCCACCCGTACCGCCAGCGTCGCCTGGGTGCCCTCGACGGTGACCCGCAGCGACAGCCCGCCCTCCGGCGGGGCCTCGCCGCCGCGGCGG
      < A  V  R  V  A  L  T  A  Q  T  G  E  V  T  V  R  L  S  L  G  G  E  P  P  A  E  G  G  R  R
24820 GAGTGGTAGCGCAACCCGAGCGCGGCCACCGCGTGCCGCCCCACGGCGTCCTCGATGTCGTACCGGTTGTAGTTGCGGCGGCCGAGGAAGGA
      <S  H  Y  R  L  G  L  A  A  V  A  H  R  G  V  A  D  E  I  D  Y  R  N  Y  N  R  R  G  L  F  S
24912 GGCGGCGACGTCCACGGTCGCCGGCCGCCCGGGCACGCCGCAGGCGGCGCGGGCCGGCAGCACCGCCGGCAGCGCCGCCGCCCGGGCCAGCC
      < A  A  V  D  V  T  A  P  R  G  P  V  G  C  A  A  R  A  P  L  V  A  P  L  A  A  A  R  A  L  R
25004 GGGTGAAGGCCGCCAGGTCCGCCTTGGTGTGGCCGACGCCGTCGGCGACGGCGACGAGCAGGAACAGGTCGTCGACGGTACGCAGATCCAGC
      < T  F  A  A  L  D  A  K  T  H  G  V  G  D  A  V  A  V  L  L  F  L  D  D  V  T  R  L  D  L
25096 AGGCGCGGCTCCGCGCTGGCGGCGGAGAACCACACCTCGCGGTGCCGGCGGTGCTCGACCCGGCCGAGGCCCCGCTCCTCGATCTCCTGGGC
      <L  R  P  E  A  S  A  A  S  F  W  V  E  R  H  R  R  H  E  V  R  G  L  G  R  E  E  I  E  Q  A
25188 GGCCACCTCCTCCAGCCCTCGCAGGGTCCGTGCCATGAAGCGCACCGTCACCGTCCGCCGATCCTCTCCCCGCCGGGTCGTCCCGCCGCC
      < A  V  E  E  L  G  R  L  T  R  A  M
25278 GTGCCGGCGGCGTCCGCGAGCCTACCCACCGCACCCGCCGCCGGGACGCAGCCGACGCCGACCGGACCCGCCGACGGGGGAGCCGACGCCGA
25370 CCGGACCCGCCAAGACTAGGTGAACCTCTATAGGAATTCGCGTGCCCCCTTCATAGGGTCCGAAAGGGGTAATGGAACCGTCCGGCACCGGA
25462 CGGCTCGTTTTCTTCCCCCAATTCCGTCCGTCCGACCTGAGCCGTCGCAGGGAAGGCGAGGCCGAGCAGTCGAGCAGTTGATCGGTCGATG
                                                                                                  > M
25553 CCGCACGGGCCCGTGCGCCGAAATCGTGGAGATTGCGCAGTGCGTACACCGGATCTGTTCATCGGCGCCGTCGGCGCCTTCGTCCCGCCGAC
      > P  H  G  P  V  R  R  N  R  G  D  C  A  V  R  T  P  D  L  F  I  G  A  V  G  A  F  V  P  P  T
25645 GGTGAGCGTCGAGTGGGCGATCGACCGCGGTCTTTACTCCCGCGAGCAGGTGGAGCTGCACGAGCTGGCGGGCACGGCCATCGCCGGCGACC
      > V  S  V  E  W  A  I  D  R  G  L  Y  S  R  E  Q  V  E  L  H  E  L  A  G  T  A  I  A  G  D
25737 TGCCCGCGCCGGAGATGGCGCTGCGCGCCGCCCAACAGGCGGTCAAGCGCTGGGGCGGCTCGCCGACGGAGTTCGACCTGCTGCTCTACGCC
      >L  P  A  P  E  M  A  L  R  A  A  Q  Q  A  V  K  R  W  G  G  S  P  T  E  F  D  L  L  L  Y  A
25829 AGCACCTGGCACCAGGGGCCCGACGGCTGGCCGCCGCACTCCTATCTCCAGCGGCACCTGGTCGGCGGCGACCTGCTGGCGTTGGAGATCCG
      > S  T  W  H  Q  G  P  D  G  W  P  P  H  S  Y  L  Q  R  H  L  V  G  G  D  L  L  A  L  E  I  R
25921 GCAGGGCTGCAACGGGATGTTCAGCGCGTTCGAGCTGGCCGCCAGCCACCTCCAGGCGGTACCCGAGCGCACCAGCGCCCTGCTGGTCGCCG
      > Q  G  C  N  G  M  F  S  A  F  E  L  A  A  S  H  L  Q  A  V  P  E  R  T  S  A  L  L  V  A
26013 CCGACAACTACGGCACCCCGATGGTCGACCGCTGGCGGATGGGCCCCGGCTTCATCGGTGGCGATGCCGGCAGCGCCCTCATCCTCACCAAG
      >A  D  N  Y  G  T  P  M  V  D  R  W  R  M  G  P  G  F  I  G  G  D  A  G  S  A  L  I  L  T  K
26105 CGACCCGGCTTCGCGCGGCTCCGCTCGGTCTGCACCAAGTCGGTCCCGGAGGCCGAGCGGCTGCACCGGGGCGACGAGCCGCTGTTCCCCCC
      > R  P  G  F  A  R  L  R  S  V  C  T  K  S  V  P  E  A  E  R  L  H  R  G  D  E  P  L  F  P  P
26197 GAGCGTCCTGACCGGCCGGGAGCTGAACTTCACCGCCCGGATCGACCAACAGTTCGCCGCCCGCAGCCCCGCCTCGATCGCCATGGCGGACG
      > S  V  L  T  G  R  E  L  N  F  T  A  R  I  D  Q  Q  F  A  A  R  S  P  A  S  I  A  M  A  D
```

Figure 11G

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26289 TCGGCGACCACATCGAGGAGGTCGTGGGGCGCGCCCTCGCCGAGGCGGAGATCGAGGTCGGCGACCTCGCCAGGGTCGCCTTCATGAACTTT
    >V G D H I E E V V G R A L A E A E I E V G D L A R V A F M N F
26381 TCCCGGGAGATCATGGAGCAGCGCTGCCTGGCCAACTGGGGCCTGCCCATGAGCCGGTCCACCTTCGACTTCGGTCGCCGGATCGGGCACTG
    > S R E I M E Q R C L A N W G L P M S R S T F D F G R R I G H C
26473 CGGGGCGAGCGACCCCTTGCTGGCCCTGGAACACCTGGCCAGGACGGGGGGCCTCGGCCCCGGCGATCACCTGCTGACCCTCGGCACCGCGC
    > G A S D P L L A L E H L A R T G G L G P G D H L L T L G T A
26565 CGGGCGTGGTGGTGTCGTGCGCGATCGTCCAGGTGATCGAGTCGCCGACGTGGCGGGAGTGACCCGCTGGACACCTGCGGCGGCCCGCCCA
    >P G V V V S C A I V Q V I E S P T W R E ∘
26656 GCCCAGCAAACCGACAGCAGGGGATGATTGTGGAAGCAGAGAAGGACCGGTTGCGTCCGGTGGCGTCCGAGGCGGTCGCCGTGGTGGGGA
                                    > V E A E K D R L R P V A S E A V A V V G
26746 TCGGCTGCCGGTTCCCGGGCGACGTCAACTCGCCCGACGAGTTCTGGGACCTGCTCACCGGGGGTCGCAACACCACCGGGACGGTGCCCGAG
    >I G C R F P G D V N S P D E F W D L L T G G R N T T G T V P E
26838 GAGCGCTGGAGCGCGTACCGCGACCTGGGTCCGGCGTTCGAGTCCGCGCTCCGGTCGGCCACCCGGGCGGGCAACTTCCTGGCCGACATCTC
    > E R W S A Y R D L G P A F E S A L R S A T R A G N F L A D I S
26930 CGGCTTCGACGCGGACTTCTTCGGCATCTCCCCGCGCGAGGCCGAGCTGATGGACCCGCAGCAGCGGCTCATGCTGGAGGTGACCTGGCAGG
    > G F D A D F F G I S P R E A E L M D P Q Q R L M L E V T W Q
27022 CGCTGGAGGACGCCGGGATCCCGCCCCGCACCCTGGCCGGCACCGACGTCGGCGTCTTCGCCGGCGTGTGCACCTACGACTACGGCGGCCAC
    >A L E D A G I P P R T L A G T D V G V F A G V C T Y D Y G G H
27114 CAGTTGGAGGACCTGCCGCACATCGACGCCTGGACGGGCATCGGCGCCGCCACCTGCGCCGTCGCCAACCGGGTCTCCCACGTGCTCGACCT
    > Q L E D L P H I D A W T G I G A A T C A V A N R V S H V L D L
27206 GCGCGGGCCGAGCCTGTCGATCGACACCGCCTGCTCGGCGTCGCTGGTCGCGTTGCACCTCGCCGCGCAGAGCCTGCGGCTGGGCGAGAGCA
    > R G P S L S I D T A C S A S L V A L H L A A Q S L R L G E S
27298 CGCTGGCCCTCGCCGGCGGGGTCAACCTGATCGTCACGCCCGGGCAGTCGATCACCCTCGGCTCGGCCGGTGCCCTGGCACCCGACGGGCGC
    >T L A L A G G V N L I V T P G Q S I T L G S A G A L A P D G R
27390 AGCAAGTCCTTCGACGCCACCGCCGACGGCTACGGTCGTGGCGAGGGGTGCGGCGTCCTCGTGCTCAAGCTGCTCTCCGACGCCCAGCGGGA
    > S K S F D A T A D G Y G R G E G C G V L V L K L L S D A Q R D
27482 CGGGGACCGGGTGCTGGCCGTGCTGCGGGGCAGCGCCGTCAACCAGGACGGCCGGACCAACGGGATCATGGCACCGTGCGGCCAGGCCCAGG
    > G D R V L A V L R G S A V N Q D G R T N G I M A P C G Q A Q
27574 AGCACGTGATGGTCCGCGCCCTGCGCTCGGCCGGCATCGAGGCCGGCAGCGTCGACTACATCGAGGCGCACGGCACCGGCACCCCGCTCGGT
    >E H V M V R A L R S A G I E A G S V D Y I E A H G T G T P L G
27666 GACCCGATGGAGGCCGCGGCGATCGGCTCGGTCTACGGGCAGGACCGCCCGGACGACGAGCCCTGCCTGATCGGTTCGGTCAAGTCCAACAT
    > D P M E A A A I G S V Y G Q D R P D D E P C L I G S V K S N I
27758 CGGCCACCTGGAGGGCGCGGCCGGCGTCGCAGGCGTCATCAAGGCGGTCCTGGCGCTGAACCGGGCCGAGGTGCCCGCCACCCTGCTGGTCA
    > G H L E G A A G V A G V I K A V L A L N R A E V P A T L L V
27850 CCGAGGTCAACCCGGACATCGAGTGGAAGCGGCTGCGGCTGCGCCTGGTCACCCGCAACCAGCCCTGGCCGGACCGGCCGGGGCCGCGCCGC
    >T E V N P D I E W K R L R L R L V T R N Q P W P D R P G P R R
27942 GCCGGAGTCTCCGGCTTCGGCTACGGCGGCACCGTGGCGCACGTGGTGCTGGAACAGGCCCCGCCGGTCGCCGCCGAGCCGGCCCCGGCGCT
    > A G V S G F G Y G G T V A H V V L E Q A P P V A A E P A P A L
28034 GACCGGCGAGACGCTGTTCCCGATCTCCGCCGGCTCCGCGCACTCCCTTCGCGAGCGGGCCCGCGCCCTGGCCGGGATCGTCCCGGATGTCG
    > T G E T L F P I S A G S A H S L R E R A R A L A G I V P D V
28126 ACCTCGCCGCGCTCGGGCACACCCTGGCTCGGCGGCGTTCGCACCTGACCCACCGGGCGGTGGCGGTGGCCGCCGGCCGGGACGACCTGGTC
    >D L A A L G H T L A R R R S H L T H R A V A V A A G R D D L V
28218 GCGGCGTTCGCGGCGCTCGCCGACGACAGGCCGCACGACCGGGTGCGTACCGGAAGCCCGGTGGCGGAGCCGCCCCGCACGGTGTGGGTGTT
    > A A F A A L A D D R P H D R V R T G S P V A E P P R T V W V F
28310 CTCCGGGCACGGGTCGCAGTGGACGGGCATGGGGCGGGAACTGCTGGCCACGGAGCCGGCCTTCGCGGACGCGATCGACCGCATCGAGCAGA
    > S G H G S Q W T G M G R E L L A T E P A F A D A I D R I E Q
28402 TCTTCCTCGACGAGATCGGTTTCTCACCCCGCCAGGCGATCCTCGACGGCGACTACGAGGCCGTCGACCGGACCCAGACAATGATCTTCGCG
    >I F L D E I G F S P R Q A I L D G D Y E A V D R T Q T M I F A
28494 ATGCAGCTCGGCCTGGCCGAGATGTGGCGAGCGAGGGGAGTCGAGCCGGACGCGGTGATCGGCCACTCGGTCGGAGAGATCGCCGCGGCGGT
    > M Q L G L A E M W R A R G V E P D A V I G H S V G E I A A A V
28586 GACCGCCGGCATCCTGACCGTGGCCGACGGCGCACGGCTGATCTGCCGTCGTTCCCTGCTGCTGCGCGAGGTCGCCGGCCAGGGCGCGATGG
    > T A G I L T V A D G A R L I C R R S L L L R E V A G Q G A M
28678 CCCTGGTGACGCTGCCCTTCGAGGAGGTCGCGGCCAGGCTGGCCGGCCGCGTCGACGTGGTCGCCGCGATCGCCTCCTCCCCCTCGTCGACC
    >A L V T L P F E E V A A R L A G R V D V V A A I A S S P S S T
28770 GTGGTCTCCGGCGACCCGGCCGCGCTGGACGCGCTGGTCGCCGAGTGGACCGAGGAGGGCCTGGGCGTACGCCGGGTCGCCTCCGACGTGGC
    > V V S G D P A A L D A L V A E W T E E G L G V R R V A S D V A
28862 CTTCCACAGCCCGCACATGGATCCGCTGCTCGACCGGCTGCGCGCCGCCGTCGACTTCACCGCCCGCGCACCCCGGGTGCCGATCTACAGCA
    > F H S P H M D P L L D R L R A A V D F T A R A P R V P I Y S
28954 CGGCGCTGGCCGACCCGCGGGCCCCGATCACCGCCGACGGCGAGTACTGGGCCGCGAATCTGCGCAACCCGGTCCGGCTCGCCGCAGCGGTG
    >T A L A D P R A P I T A D G E Y W A A N L R N P V R L A A A V
29046 GCCGCCGCCGTCTCCGACGGACACCGGGCCTTCATCGAGGTCTCCCCGCACCCGGTGGTGACCCACTCGATCCACGAGACGCTGGCCGGAAG
    > A A A V S D G H R A F I E V S P H P V V T H S I H E T L A G S
29138 CCTCGACGACGAGGTCTTCGTCGGCGGCACCCTGCGCCGCGACACCCCGGAGGCGCAGGCCTTCCTGTCCAGCCTGGGGGCCGCGCACTGCC
    > L D D E V F V G G T L R R D T P E A Q A F L S S L G A A H C
29230 ACGGGGTCGCGGTCGACTGGGGCCGGGTGCATCCGTCCGGGCCGCTGGTCACCCTGCCCGGCTACCCCTGGCGGCACCGGAGTCACTGGCAC
    >H G V A V D W G R V H P S G P L V T L P G Y P W R H R S H W H
29322 TGGCCGACGCCGGCCGCCGCCACGGGCCGGGGCCACGACCCCGCGTCGCACACCCTGCTCGGCGCGGTCGACAACGTGGCGGGCAGCGACGT
    > W P T P A A A T G R G H D P A S H T L L G A V D N V A G S D V
29414 GCGGGTGTGGCGCACCGCACTCGACGACGCCAGCCGCCCGTACCCGGGCAGCCACGCCCTCAACGGCGTGGAGATCGTTCCGGCGGCCGTGC
    > R V W R T A L D D A S R P Y P G S H A L N G V E I V P A A V
29506 TGGTGGAGACCCTCATGGCTGCCGCCGGGCGGGGCGACGGCCGGCCGCTGCTGACCGGCTTGTCGATGCGGTACCCGCTGATGACCGCCGGG
    >L V E T L M A A A G R G D G R P L L T G L S M R Y P L M T A G
29598 CTGCACGAGGTCCAGGTGGTGCGGGACGGTGCCGAGGTGCGGCTGGCGTCCCGTTCCGTCGACGCGGAGGCCGACCCGAGCCGGGACTGGCT
    > L H E V Q V V R D G A E V R L A S R S V D A E A D P S R D W L
29690 GATCCACACCGACGCCACGGTGGCCGACGCCGACGCCACGGTGCTCGCCGCGCGGGCGTTGGCCGACCCCGACGACCACCGGATGGAACCGG
    > I H T D A T V A D A D A T V L A A R A L A D P D D H R M E P
29782 GCGACCCGGGCTCCATCCACCGCCGGCTCGCCGAGGTCGGGGTGCCGTCGACGGGATTCGACTGGTCGGTGGAGGAGCTGCTCTCCGGGTAC
    >G D P G S I H R R L A E V G V P S T G F D W S V E E L L S G Y
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Figure 11H

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29874 GGCGTGCTCCGCGCGCGGGTGCGCTCGGCCGACTCGTCCACCTGGGCGCCGGTGCTGGACGCCGTCATGTCGGTCGCCCCCGCCGTCTTCCC
      > G V L R A R V R S A D S S T W A P V L D A V M S V A P A V F P
29966 CGGCGTGCCGCAGCTACGCATGGTGGTGTACGTCGACGAGGTGCTGCTCACCGGCGAGCCACCGGAGGTGACGCTGATCGAGGTCGCCCTCG
      > G V P Q L R M V V Y V D E V L L T G E P P E V T L I E V A L
30058 ACCCAGACCGGCCCGACACGGCGAACGCGCTGGTCGCGGATGCTCAGGGCCGGGTCGTGGCCAGCCTTCCCGGGCTGCGCTACCCGGTGATC
      >D P D R P D T A N A L V A D A Q G R V V A S L P G L R Y P V I
30150 GACCAGCCGGTCGCCCCGGCGCAGGACAGTTCCGGCGAGGTGGAGGAGGCGGTCTCCTTCGCCGGCCTGTCCGACGAGGAACTGCACGAGCG
      > D Q P V A P A Q D S S G E V E E A V S F A G L S D E E L H E R
30242 GGTGTTCGACGAGGTGCGCCGGCAGATCGCCGGGGAGATGCGACTCGACGCCGACGACCTGCATCCCCGCCGGCCGCTGGCCGAGCAGGGCC
      > V F D E V R R Q I A G E M R L D A D D L H P R R P L A E Q G
30334 TCGACTCGGTGATGACGGTGGTGATCCGGCGACGCCTGGAGAAGCGCACCGGGCGGAGCCTCTCCCCGACCGTCTTCTGGCAGCGGCCCACC
      >L D S V M T V V I R R R L E K R T G R S L S P T V F W Q R P T
30426 GTCGCCGCCATCGCCGACCACCTGGTGGAGCTGTTGAGCACCCCGCAGGAGTGAGGATCCGCGACGACAGGGAGGGCCCGTGCGTTCCGCA
      > V A A I A D H L V E L L S T P Q E ∘
30517 CGGGCCCTCCCTGCTGTCGACGGATCTTCAGGTGGCGGGGTCAGCCCGGCCGCTGGTCCACCGCAGGGGTGGCGGCCCACTCCAGGTGGCG
                                          < ∘ G P R Q D V A P T A A W E L H R
30608 GCTCTCCCGCAGGGTCTCCTCGGCGTTCTGTTCGACCCGCCGCATGGCGACGCGCAGCATCGGCGGCGCCATGACCGAGGTGACGACCGCGA
      < S E R L T E E A N Q E V R R M A V R L M P P A M V S T V V A V
30700 CCAGCACCACGATGGTGTATGAGGCGGTGTTCAGCACGCCCAGGCGCAGCCCGACCATCGCGATGATGATCTCCACGGCACCGCGCGCGTTG
      < L V V I T Y S A T N L V G L R L G V M A I I I E V A G R A N
30792 AGCCCGGCGCCGAGGGCGACGCCCTCCCAGTGGCTCTGCCGGGCCAGCCGTGCACCCAGGTACGCGCCGGTGTACTTGCCGAGCACGGCGAG
      <L G A G L A V G E W H S Q R A L R A G L Y A G T Y K G L V A L
30884 CGCCAGGATCACCGCCCCGGCGGCGAGCACCTCCGGGTCGGCGAGGGCACGCAGATCGACCCGGAGCCCCGCGCTGGCCAGGAAGATCGGGG
      < A L I V A G A A L V E P D A L A R L D V R L G A S A L F I P A
30976 CGAGCACGGACAGCACCACCGTGCGCAGCGGTGCCAGCCGGGCCGGCTCCCCGTTGCCGGGAAGGCCGATCAGGACACCCGCCACCAGCGCG
      < L V S L V V T R L P A L R A P E G N G P L G I L V G A V L A
31068 CCGAAGATCGCCTCCAGGCCCAGCGCGTCGCCCCCGCCGCGAAGGCCAGCACGATCACCACGGCGACGGCGCTGGCGGCCCCGCCGTCGGG
      <G F I A E L G L A H A G A A F A L V I V V A V A S A A G G D P
31160 CTGGGCGTTCGCCCAGCGCATGGCGCGCCGGGTCACCGGCCGGCCGACCAGGACGGCCACCGCGAGGTAGGCCACGAGGTAAAGCAGGGCGG
      < Q A N A W R M A R R T V P R G V L V A V A L Y A V L Y L L A T
31252 TCACCACCTGCCCGGCGGTGAGGGTGCTCACCGCCACCGACGAGATGAGCGACAGCAGGAACCAGGCCGCAGCGTCCTCCAGCGACGCCGCA
      < V V Q G A T L T S V A V S S I L S L L F W A A A D E L S A A
31344 GCCAGGATGATCTGCCCCACGTCGCGGTGCAGCAGGCGCATGTCGGTGAGCGTCTTCGCGATCACCGGCACGGCGCTGACCGCCATCGCCAC
      <A L I I Q G V D R H L L R M D T L T K A I V P V A S V A M A V
31436 GCCGACGAACAGCGCGAAGACAGTCCGCTCCTGCCCGGCCGCGAGAAGCGCCGCCGGGGCCAGCAGGCCGGCGGCGATGCCCAGGCCGAGGG
      < G V F L A F V T R E Q G A A L L A A P A L L G A A I G L G L P
31528 GCACCGCGAGGCCGCCGACGGCCACCGCGCCGATCGTGCCGGCCCGCCGCCGGACCAGCCGCAGGTCCAGGTGCAGACCGGCCACGGCGACC
      < V A L G G V A V A G I T G A R R R V L R L D L H L G A V A V
31620 AGCAGTACGACGCCGAACTGACCGATGGCGTCGAGCAGGTGGACCTGGTCGGGGTCGGCGGGCAGCAGCCACCGTCCGATGTCGGGTGCCAG
      <L L V V G F Q G I A D L L H V Q D P D A P L L W R G I D P A L
31712 GGCCCCCAGCACCGAGGGGCCGAGCAGCACCCCGGTCAGCAGCTCACCGACCACCGCCGGCAGGCCGAAGCGTTGCGCCACCCGTCCCAGGA
      < A G L V S P G L L V G T L L E G V V A P L G F R Q A V R G L V
31804 CGACGGCGAGCAGCAGCAGGCCCACCTGGAGCAGGAACAGCAGTAGCTGGTGGGAGCCCAGCGGGGGCACCGGCGCGGCCACGATCA
      < V A L L L L L G V Q L L F L L L Q H S G L P P V
31894 CGGTCGTTGTTCCTTTCGTCTCGACGCCCGGCCGGGCCCGCCGGTGGTCAGGCCGCGATCTCGGGCGGCAGGTCCACCGGGTCGGCCGAGT
                                                  < ∘ A A I E P P L D V P D A S N
31985 TCATGAAGGTCCGCAGGGCCCGCAGGTCGGCGGCGGGCTTCTCCCAGCCCAGCCCGGCGCACCAATCGATGAGGGAGGTCAGCTCCCCGGTG
      < M F T R L A R L D A A P K E W G L G A C W D I L S T L E G T
32077 GCCCGAACCTTGTCCTCCTCGGGCAGGCTGAGCACCGACATCTCGGCCGGCCACTGCACCACGTTGGCCAGGTCCACGTCGAGCCCCTCGGC
      <A R V K D E E P L S L V S M E A P W Q V V N A L D V D L G E A
32169 CCGGGCGAACTCCAGCAGGTCGCGCAGCCCCCAGACGTTGTCCCGCTGGGGTGCCACCTGGAGCCAGAGGTTGACCTCCGAGCGGGCCCGGC
      < R A F E L L D R L G W V N D R Q P A V Q L W L N V E S R A R R
32261 GGACGTTCGCGATGAAGGTCTCCCACTTCGCGCCCTGCCGGATCCGCTCGAACACCTCGCCGTAGCCGTCGCAGGAGGCGCCGATGCCGATG
      < V N A I F T E W K A G Q R I R E F V E G Y G D C S A G I G I
32353 CTCTTGAAGTGCCGGAACCGGTCGAAGACCGACTCCGGCAACACGGTGAGGTTGGAGTTGTAGACGACGTCGACGTTGCCGGCGTTACCCGT
      <S K F H R F R D F V S E P L V T L N S N Y V V D V N G A N G T
32445 CTCCACCAGCAGGTCGAGCAGGGCGAAGTGGCCCGGCTGCATGAACGGCTCCCCACCGGCGAAGTACAGCCGCCGGATGAGGTGGGCGTTCT
      < E V L L D L L A F H G P Q M F P E G G A F Y L R R I L H A N E
32537 CGCGCAGGGTCTGCCACAGCTCGTCGTCGTCCCGGTAGGCGTCGATGACCGCGGACGACCAGGCCGGCCGCTTCTTGGCGCCCCAGCCCGAG
      < R L T Q W L E D D D R Y A D I V A S S W A P R K K A G W G S
32629 CTGACCGGGTACGCGCACATCACGCACCGCAGGTTGCAGGTGTTGCCGAACCGGATGTCGAGGAAGAACGGGAAGTCCTCGACGGTGCCGTC
      <S V P Y A C M V C R L N C T N G F R I D L F F P F D E V T G D
32721 GGGCGCGGTGCGGGCGGCCAGCCGGTCGGGGTCGGCGATGTCCCGGAACCGCTGGTTGATCTCCTGCCGGTACGACAGCGCGCCGTGGTCCT
      < P A T R A A L R D P D A I D R F R Q N I E Q R Y S L A G H D E
32813 CGCGGTGGTAGCAGTAGGAGCAGGCGTCGACCCGCTCCCCGGCCAGCATCGCCAGCCGGGTCCGGCGCATGTTGGGGCTGTTGAAGGCGTC
      < R H Y C Y S C A D V R E G A L M A L R T R R M
32904 CGCCAGGCCCATCACCCGGCCGGGGTTGTCCGCCGCGTAGCGGGACCGCGGCGAGCAGCCGACGGCGTCGTCGTTGAGCAGGAACTCCGGCT
32996 CCTCCTCCTGCTCGTACAGCTTGTTGTGGTACATCGAGTCGTCCACGCAGCACCGCCCGTAGACACCGTCGATGGACGCGCAGAGATGGATC
33088 CAGGGCAGCACGCACATGGTCCGGGACCGGGCTTCCGGGTCAGTCATGAAAGTTGATCACCTCGGTGGTGGGGGCGGTGTCATCCCGGTCG
                                                                  < • G P R
33179 GCCGACCGTCTCGACCCGGGGCAGCGGAAAGATCAACCGGGTGCCGCTGGCCAGCATCTCCGCCTCCCGGGCGACGATCTCGTCCCGGAAGT
      < G V T E V R P L P F I L R T G S A L M E A E R A V I E D R F H
33271 GCCAGGGCAGGACCAGGTAGTAGTCCGGGCGGGCCGCCCGCGACTCCTGCTCGCTGATGATTTCGATGTCCGTGCCGAGGGTGCGCGCGCCC
      < W P L V L Y Y D P R A A R S E Q E S I I E I D T G L T R A G
33363 ACCTTGTCCGGATTGCGCTCCGCGGCGTACCGGATGAGCTCGCGGTCTATGCCGCAGAACTGCAGGAGGGTGTTGCCCTTCGTCGACGCGCC
      <V K D P N R E A A Y R I L E R D I G C F Q L L T N G K T S A G
33455 GTAGACGTGCACCGTGCGGCCCTGGCCCCGCAGCTCGCGCAGCAGGGCGCTCACCTCGTCACGGTGCTGGCGCACCTGCTCGGCGAAGCGCT
      < Y V H V T R G Q G R L E R L L A S V E D R H Q R V Q E A F R Q
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Figure 11I

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33547 GGTACGGGGCGTCGCCGTCCAGCCCCAGCGCCAGCTCCCGGTCGGCGAGTGCCTTGACCGAACCGTCGGCCCGGCCGCCCACCTCACCGGCC
      <  Y  P  A  D  G  D  L  G  L  A  L  E  R  D  A  L  A  K  V  S  G  D  A  R  G  G  V  E  G  A
33639 CGGGTGACCACGCAGCAGATCGAGCCGCCGTTCACCCCGTTGAGGCTGGCACGGACGATCTCCAGGCCCGCCGCGCCCAGAATGCGGCTCAG
      <R  T  V  V  C  C  I  S  G  G  N  V  G  N  L  S  A  R  V  I  E  L  G  A  A  G  L  I  R  S  L
33731 CGTGGCCAGCGAGTAGTAGGACAGGTGCTCGTGGCAGATGCTGTCGTAGCCGGCGATCTCCAGCATCGCCGGCAGGTAGGCGACCTCGACCA
      <  T  A  L  S  Y  Y  S  L  H  E  H  C  I  S  D  Y  G  A  I  E  L  M  A  P  L  Y  A  V  E  V  V
33823 CCCAGACCCCGCCCGGGGCGAGCAGCGCCTCGACCTGACGGGCGAACTCCACCGGGTCCTCGACGTCGTAGAACATCGCGATCGAGGTGACC
      <  W  V  G  G  P  A  L  L  A  E  V  Q  R  A  F  E  V  P  D  E  V  D  Y  F  M  A  I  S  T  V
33915 AGGTCGAAGCTGCCCGCGTGCGGGACCAGCTCGGGGCTGGGGAAGAAGTCGCGGATCAGATTGAAGTCGTCGGGCGCGTCGTCGGCGGCGCT
      <L  D  F  S  G  A  H  P  V  L  E  P  S  P  F  F  D  R  I  L  N  F  D  D  P  A  D  D  A  A  S
34007 GGAGGGGTCGATGCCCCACCGCTGCGCGTCGGTCAGGTTGCCCAGCAGGGTGCCGTCGTTGCAGCCGATGTCGAGCACCTTGCCGGGCCGCT
      <  S  P  D  I  G  W  R  Q  A  D  T  L  N  G  L  L  T  G  D  N  C  G  I  D  L  V  K  G  P  R  E
34099 CCCCCAACACCTCGACCGCCGCGTCCACGACGTCGGCGAGATGCCGGCGCATCGTGTCGTTGATCCGCGAGCGGTACCAGTAGGTGTCGTAG
      <  G  L  V  E  V  A  A  D  V  V  D  A  L  H  R  R  M  T  D  N  I  R  S  R  Y  W  Y  T  D  Y
34191 AGCAGCCCACCCGGCAGGGTGTGCCGCAACTGCACCAGGCCGCACGGGTCACCGCCGTCGCGTTCCGCGCACCGGGTCAGCTCCAGGGGGAA
      <L  L  G  G  P  L  T  H  R  L  Q  V  L  G  C  P  D  G  G  D  R  E  A  C  R  T  L  E  L  P  F
34283 GCGCACCCTGGGCGGGTCCGACACGCCGGGCTTCACGAAGCTGCCCTGTAGGTACTGGGCACCGAGGTCGAGGACCGTACGCAGGGTCCCGC
      <  R  V  R  P  P  D  S  V  G  P  K  V  F  S  G  Q  L  Y  Q  A  G  L  D  L  V  T  R  L  T  G  G
34375 CACACACCCGGCAGGTGGTCCGCTCGACCACCTCCGACGCCAACTCCTCGCCGGCCGCCGCCAACTGGCTCACGTCAGGTCCTCCTCGT
      <  C  V  R  C  T  T  R  E  V  V                                                  <  •  T  R  R  T
34464 CTCGTGCCGGTGTGCGGGACCAGGCGCCCCGTCGTGCGGTTTGCTGGCGACCAGCAGGATGTCCAGATAGAAGGGCTGGTCGGGGCCCTCGC
      <  E  H  R  H  A  P  G  P  A  G  D  H  P  K  S  A  V  L  L  I  D  L  Y  F  P  Q  D  P  G  E  S
34556 TGCGGCCGAGATGCCGGAACGCCCGGTCGAGGTACTCGTCGAGCGCGCGGGGCCGCAGCCGGTCCACCAGCCACAGGGCGCGCAGGGCCAGA
      <  R  G  L  H  R  F  A  R  D  L  Y  E  D  L  A  R  P  R  L  R  D  V  L  W  L  A  R  L  A  L
34648 CCCACCGGGCCGCCGGACGGCCAGCCGTGCTCGCGGCCGTACCAGCGCAGCAGCAGCAACAGGCCGCGCGGCCCGCAGGTCAGCTTGACGGT
      <G  V  P  G  G  S  P  W  G  H  E  R  G  Y  W  R  L  L  L  L  L  G  R  P  G  C  T  L  K  V  T
34740 GCGGTCGACGGTGAAGCCGGCCCACTCGGCCTGGCGGGCCAGCCCGTCGGCGGTCCACCGCCACAGGTCCTGGCCGCCGTGCTCCTCCCACA
      <  R  D  V  T  F  G  A  W  E  A  Q  R  A  L  G  D  A  T  W  R  W  L  D  Q  G  G  H  E  E  W  V
34832 CCCCGTGGGTGGAGAGCACCAGCCGGCCGCCCGGGCGCAGCAGCCGGTACGCCTCCCGCAGGTACGCGTCCGCGTCCGAGACGTGTTCGAGC
      <  G  H  T  S  L  V  L  R  G  G  P  R  L  L  R  Y  A  E  R  L  Y  A  D  A  D  S  V  H  E  L
34924 ACCTGGGTGGAGAGCACCCCGTCGAACGTCCCGTCCGGCACCGGGCAGCGCCCGTCCCGGTCGAGGGCGTGGTCGGCCGGCAGGGACTCACC
      <V  Q  T  S  L  V  G  D  F  T  G  D  P  V  P  C  R  G  D  R  D  L  A  H  D  A  P  L  S  E  G
35016 GCCCGGGATGTCGGCGGTCTGCAACTCGGCGGAGCGGAACAGGCCCCGGTATGGCGAGGTGCCCGCGCCGTAGTCGAGCCAGACTCCCGTGG
      <  G  P  I  D  A  T  Q  L  E  A  S  R  F  L  G  R  Y  P  S  T  G  A  G  Y  D  L  W  V  G  T  A
35108 CGTCCCGGACCGCCTCCGCCAGCGCGTCGCGCAGGTCCAGGAAGTGGGCGTATGCCCAGTCCCCGGGCCGGGGCTCGATCCGCTCCCGGAAC
      <  D  R  V  A  E  A  L  A  D  R  L  D  L  F  H  A  Y  A  W  D  G  P  R  P  E  I  R  E  R  F
35200 CGTTCGGCCATCACCTCGTCCAGCGACGGGCCGGTGGGGGCGGTGCCGGCACCGGTCAGCAGGGGACCAAGCCCGGGTACGCGCCGCAGC
      <R  E  A  M
35290 AGGGTCACCAACGCCAGTACTCCTCGTGCGGGTACCGCATGGTGGTCGGCTCCGGCAGGCCCTCCCAGCGCCGCAGCGACGCGGCGGGCCG
         <  •  W  R  W  Y  E  E  H  P  Y  R  M  T  T  P  E  P  L  G  E  W  R  R  L  S  A  A  P  R
35381 GTACTCGAAGGGCTGCTCGCCGGCGTGCTCCGGTGCCGCCCGCCGCTGCGCCAGGCAGGAGAGCAGCACCTGCTGCTTGAGCCCGATGTACT
      <  Y  E  F  P  Q  E  G  A  H  E  P  A  A  R  R  Q  A  L  C  S  L  L  V  Q  Q  K  L  G  I  Y  E
35473 CCGGCACGTGCGGGCCGAGGTCCAGCTCGACCTCGGCGGGCCGGTACTCGAAGTAGATGACCCGGCGCCGCTTGCCGGTCACCGCCGGCGCG
      <  P  V  H  P  G  L  D  L  E  V  E  A  P  R  Y  E  F  Y  I  V  R  R  R  K  G  T  V  A  P  A
35565 GCGTGCAGCATCAGGATGTTGTGCAGCATCACGTCGCCCGGGTTCATCACCGCCGGCACCGCCCCGGTGGTGTCCCACTCGGTGGCGTTCAT
      <A  H  L  M  L  I  N  H  L  M  V  D  G  P  N  M  V  A  P  V  A  G  T  T  D  W  E  T  A  N  M
35657 CCGGGTGGTGGTCTCGTTCGCCCGGTCGGTGTCCCAGTAGTTCGACTGCGGGATGCACCAGACGCAGTTGTCCTCCGGGGCCGGGTCAAGGT
      <  R  T  T  T  E  N  A  R  D  T  D  W  Y  N  S  Q  P  I  C  W  V  C  N  D  E  P  A  P  D  L  Y
35749 AGATGCCGACGTCGATCACCCGGCCCGCGCCGGTGATGCCGACCGCGTTCTCCGGGTAGAGGCCGCCGTCGCGGTGCCAGGGCAGCCGGGGC
      <  I  G  V  D  I  V  R  G  A  G  T  I  G  V  A  N  E  P  Y  L  G  G  D  R  H  W  P  L  R  P
35841 GCCCCCGCCTCGGTCTTGAAGACCATGCTGTCCCAGGTGGGGATGAGGTTGGGGCCGACCAGGTCCTCCATCGCCCGCAGCAGCAGGGGGTG
      <A  G  A  E  T  K  F  V  M  S  D  W  T  P  I  L  N  P  G  V  L  D  E  M  A  R  L  L  L  P  H
35933 GCCGGCGAGCCGGGCGACCACCGGGGACTTGTCGACCACGTACTCGATCCGCACCGGCGCCGCGTCCGGCTCGTGCGGTTCCAGCGTCCAGA
      <  G  A  L  R  A  V  V  P  S  K  D  V  V  Y  E  I  R  V  P  A  A  D  P  E  H  P  E  L  T  W  I
36025 TGGTGTCGGTCATCGTCCGGGTGCGCCAGGCTTCGTCGATCAGCTCGTCGGCCGCCGCCTGCACGGACCGCAGCTCGTCGGGGTCCAGCAGC
      <  T  D  T  M  T  R  T  R  W  A  E  D  I  L  E  D  A  A  A  Q  V  S  R  L  E  D  P  D  L  L
36117 CCGCGCAGGATCAGCGCGCCCTGCCGGCGGAAGGCGGTCAGGTGCTCCGGAAGCAGCCCGGTCTCGTGGATGTGGCACTCGGGGACGGCCTG
      <G  R  L  I  L  A  G  Q  R  R  F  A  T  L  H  E  P  L  L  G  T  E  H  I  H  C  E  P  V  A  Q
36209 CTCGGTGCGGACGTCCACAGTCGCGCTCATGGTTCGGTTCCCTTCTGCCAGGCGGACGGTTCGTGCTGCCCGGAGCCGCCGGCCGGGCCCG
      <  E  T  R  V  D  V  T  A  S  M
                                     <  •  P  E  T  G  K  Q  W  A  S  P  E  H  Q  G  S  G  G  A  P  G  P
36300 GGCTCGGTCGGTCGGCGACGAAGTACCAGTGCTCCCGCAGCGCGTCGGCGAACCCCGCCCGGTCCAGCGCCGGCTGCCCGGCGCGGCGCCCG
      <  S  P  R  D  A  V  F  Y  W  H  E  R  L  A  D  A  F  G  A  R  D  L  A  P  Q  G  A  R  R  G
36392 GGCAGGGTACGCAGCTCGTAACCCAGCTCGGTCACGAGCAGCGCCCACAGGTCGGCGCTGGTGGTGCCGTACTCCCGCATGGCGTGGTCGCC
      <P  L  T  R  L  E  Y  G  L  E  T  V  L  L  A  W  L  D  A  S  T  T  G  Y  E  R  M  A  H  D  G
36484 GCCGTGCTCGAAGACGATCACCGGCCGCCAGCGGCGGAGCAGCTCCACGGCACCGCGCAGGGCGAGCACCTCGCCGCCCTCGGTGTCCACCT
      <  G  H  E  F  V  I  V  P  R  W  R  R  L  L  E  V  A  G  R  L  A  L  V  E  G  G  E  T  D  V  K
36576 TGACCAGGTCGATCCGGCGGTCACCGGGGAGCACGTCGTCCAGGCGGACGGTGTCGACCGTCAGCTCCCGCAGGGTCTCGTCCGGGCGGTCG
      <  V  L  D  I  R  R  D  G  P  L  V  D  D  L  R  V  T  D  V  T  L  E  R  L  T  E  D  P  R  D
36668 TAGGGACGCCGGCGCAGCCCGCTGTAGCCGGGGTTGGAGACCACGTGGACGAAGCTGTCCCGGCCGGTGCGCTCGGCGGCGGCGGCGGCCAC
      <Y  P  R  R  R  L  G  S  Y  G  P  N  S  V  V  H  V  F  S  D  R  G  T  R  E  A  A  A  A  A  V
36760 CACCGTCACGCCGGGGAAGTCCCGGCGCAGCCCCTCGGCGTACGACGGCAGCGCCTCGACGGCCACGTGCCGGCCACGGGGGGCGACCCGCA
      <  V  T  V  G  P  F  D  R  R  L  G  E  A  Y  S  P  L  A  E  V  A  V  H  R  G  R  P  A  V  R  L
36852 GCAGGTGACGCAGGATGTCGCCGGCGCCGGCCCCGATGTCCACGGTGTTGGCGTCCGGTTCGCAGATCTGCTCGATCAGCGCCACGGTGAGC
      <  L  H  R  L  I  D  G  A  G  A  G  I  D  V  T  N  A  D  P  E  C  I  Q  E  I  L  A  V  T  L
36944 TGGTCGTACCAGTCGTTCATCGACAGCGCGCCGGCCTCGTCGGTCGCGGAAAGCTCAGTGGACATCGTCACGCTCCTCGGTCCGGCACGCC
                                                                                  <  •  H  V  D  D  R  E  E  T  R  C  A
      <Q  D  Y  W  D  N  M
```

Figure 11J

```
37035 GGTCCGGCCCCGGAGCCGACCGCCGGGGCGGTACGGACCAGGAGTTCCAGCTCCCGCAGCTCGATCTCGGACAGCTCCAGGCCGGCGGCGCG
     <P  G  A  G  S  G  V  A  P  A  T  R  V  L  L  E  L  E  R  L  E  I  E  S  L  E  L  G  A  A  R
37127 GACGTTCTCCTCGACGACTCCGGGCGACTGAGCGCCGAACACCGGCACCACCCCGGCCGGGTGGTGCAGCGCCCAGGCCAGTGCCACCTGCG
     <  V  N  E  E  V  V  G  P  S  Q  A  G  F  V  P  V  V  G  A  P  H  H  L  A  W  A  L  A  V  Q  A
37219 CGACGGTGTGCCCACGCTCGGCGGCGAAGGCGGCGAGGCCGTCGACCACGTCGAGCAGTTGGGCGTAGTCCTCACCCCGGAAGGCGTGCGAG
     <  V  T  H  G  R  E  A  A  F  A  A  L  G  D  V  V  D  L  L  Q  A  Y  D  E  G  R  F  A  H  S
37311 TAGGCCCGCCAGTCCTCGGGGGCGAATGCCTGGTCGCGGTGCAGCGCGCCGGTGAGCAGCCCGTGGGCGAGCGCGGAGCCGCCCAGCACCCC
     <Y  A  R  W  D  E  P  A  F  A  Q  D  R  H  L  A  G  T  L  L  G  H  A  L  A  S  G  G  L  V  G
37403 GACGCCGGCCTCCTGGCAGCGGGGCAGCACCTCCTTCTCGGCACCACGGTCGAGCAGGTTGAACGGCACCTGGACGACGTCCAGCAGCCCGG
     <  V  G  A  E  Q  C  R  P  L  V  E  K  E  A  G  R  D  L  L  N  F  P  V  Q  V  V  D  L  L  G  T
37495 TCGGCACCAGCTCGGCCAGGTCGCCCGCCGTCACGTTGGCGAAGCCGACATGGCGGGCCAGGCCCTCGCGCACGAACCCCGCCAGCACCTCG
     <  P  V  L  E  A  L  D  G  A  T  V  N  A  F  G  V  H  R  A  L  G  E  R  V  F  G  A  L  V  E
37587 GCGGTCTCCGCGAGCGGGACGGTCGGGTCGGGCCAGTGCACGGAGTACACGTCGACGTGGTCCGTGCCGAGCTGACGCAGGCTGGCCAGCAG
     <A  T  E  A  L  P  V  T  P  D  P  W  H  V  S  Y  V  D  V  H  D  T  G  L  Q  R  L  S  A  L  L
37679 CTCGTCCCGGAGGAACGCGGGGTCGCTGTTACGCACCGTCCGTCCGGGCGGGTCGAGCTTGTGCCGTCGCACGCCGGGCCGGGTCTCCAGCC
     <  E  D  R  L  F  A  P  D  S  N  R  V  T  R  G  P  P  D  L  K  H  R  R  V  G  P  R  T  E  L  G
37771 CGCCGGCCGTGGCGATCACGATCTCGTCCCGGTGCGCGGGCAACAGGTCGGCCAGCCCGCGGGCAAGGGCCGCCTCGGCGGCCCCGCCGCCG
     <  G  A  T  A  I  V  I  E  D  R  H  A  P  L  L  D  A  L  G  R  A  L  A  A  E  A  A  G  G  G
37863 TACGCCCGGGAGGTGTCGAAAAGGGTGACGCCCAGGTCGAAGGCCCGGCGGACGGCCTGCACGCCTGGTTCGATCCGCCGGCCCCACTGGCC
     <Y  A  R  S  T  D  F  L  T  V  G  L  D  F  A  R  R  V  A  Q  V  G  P  E  I  R  R  G  W  Q  G
37955 GCCGAGCGCCCAGGTGCCCAGGCCGAGCGCCGAGACCAGCGGCCCCCGCTCACCGATGCAGCGCTGCCGCACGGCGTCCTCCCGCCCGGTG
     <  G  L  A  W  T  G  L  G  L  A  S  V  L  P  G  R  E  G  I  C  R  Q  R  V
38046 CCCCACCCACGCCCGTCGGCCGGCCGTCACGCCGCCGGCTCCCCGTCGCTGCGCAGCGTCAGGAACACCACGCCGTCGTGATTGATCATCT
                                 <  o  A  A  P  E  G  D  S  R  L  T  L  F  V  V  G  D  H  N  I  M  K
38137 TGTCGGTGACCGGCGTCAGCCCGGCCTCGGCGGCGATGCCGGTCATCAACTCCACGCCGTGCCAGTTCAGGAACCCCTTGAACTCCACGGGG
     <  D  T  V  P  T  L  G  A  E  A  A  I  G  T  M  L  E  V  G  H  W  N  L  F  G  K  F  E  V  P
38229 TTCGCGTCGCGGTACCGCTCGGCGTAGGTGTGGAAGAAGCCGCGCGTGTTGTCGCCGAGGTCCAGGAAGTTGAAGCAGAACAGCCCGCCGGG
     <N  A  D  R  Y  R  E  A  Y  T  H  F  F  G  R  T  N  D  G  L  D  L  F  N  F  C  F  L  G  G  P
38321 CCGCAGGATCCGCCGGATCTGACGGAAGTAGAGGAAGACCTCGAAGACGTTGAGGTGGATGAACACGTTCAGGGAGAACCCGGCGTCGAACG
     <  R  L  I  R  R  I  Q  R  F  Y  L  F  V  E  F  V  N  L  H  I  F  V  N  L  S  F  G  A  D  F  A
38413 CGGCGGTCGGCAGCTTCTCCAGGAAGTCGTTCTCGATGTGGTGGTAGGAGACGTTCTCCCGGCCCTCGCAGGTGGCGCGCGCCTTGTCGAGG
     <  A  T  P  L  K  E  L  F  D  N  E  I  H  H  Y  S  V  N  E  R  G  E  C  T  A  R  A  K  D  L
38505 AAGGATCGGCTGACGTCGGCGCAGAGCACGGCGCGCACCCGGTCGGCGAGCCCGGCCGCCATGATGCCCTCGCCGCTGCCGATCTCGAAGAT
     <F  S  R  S  V  D  A  C  L  V  A  R  V  R  D  A  L  G  A  A  M
38597 CTCCGATTCCGGGCCGAGCCCGAGCTGCTCGACGACCAGGGCGACCTTGTCGACACGGTCCTGGAGGTACTCCTCGCGCGGCTGGTAGCCGG
38689 CGAGCTGCATCTGCATCTCCTCCGGCGTGTTCCACTCCCAGACGTAGTTGAGGTCGCCGGTGCTCCGGAGCGGACAGCCCCGGGGGGCGTCC
38781 TGCGGCGGCGGCGTCGCCTGCTTCGCGTCGTTCATCGGACCTCACTCGCGGTCTTGTCGGGCTCTGCGGGGACAACTGGGCGGGCGGCTGCG
38873 GAAAACTGGGCGGGCGGTGTCACGGACGCCGGGCGAACTCGGCGACGTCCTCGGGGCTCAGCGCGCCGGTGTCGGCCAGCGCGGGCCAGGAG
                                <  o  P  R  R  A  F  E  A  V  D  E  P  S  L  A  G  T  D  A  L  R  A  L  L
38964 TTCGGCCACCTGGACGGCGGTCGGCCCGGTGGTGACGGACTCCCGCATCCGCTGCGCCGCCACCCGGAATCGGTGGTCGTAGAGGACGGAGC
     <  E  A  V  Q  V  A  T  P  G  T  T  V  S  E  R  M  R  Q  A  A  V  R  F  R  H  D  Y  L  V  S  G
39056 CGAGGGCCTCGTCGACCTCCTCGCGGGACGCCTTCAGGCCGGGCAGCGTCTTCGTCGCGCCCTGCGGGTCGAGCCGCCGCCCGTAGATCAGG
     <  L  A  E  D  V  E  E  R  S  A  K  L  G  P  L  T  K  T  A  G  Q  P  D  L  R  R  G  Y  I  L
39148 GCGTCGTAGTTGAGCGCCAGCGACAACTGCGGCACGCCCATGGCGAGCCCGTTCATGTAGCAGTTGGCGCTGCCGTGGTGCACCAGCAAGTC
     <A  D  Y  N  L  A  L  S  L  Q  P  V  G  M  A  L  G  N  M  Y  C  N  A  S  G  H  H  V  L  L  D
39240 GCAGTCGGGGAGGATGAGCTCCAGCGGGCAGTTGCTGAGCACCCGCACGTTCGGCGGCAGCGCGCCCAGCCCCTCCACCTCGGAGGAGGCGG
     <  C  D  P  L  I  L  E  L  P  C  N  S  L  V  R  V  N  P  P  L  A  G  L  G  E  V  E  S  S  A  A
39332 CGGTGATCACGACCTCCACGCCCCGCTGGGCGGCGGCGTCGACGGCGTGCCGCAGCGCCGGCACCTGCGCGCCGAACACGCCCGTGGCGGAG
     <  T  I  V  V  E  V  G  R  Q  A  A  A  D  V  A  H  R  L  A  P  V  Q  A  G  F  V  G  T  A  S
39424 TTGCCCCACACCACGCAGACCCGCTTGCCCCGGCGCGGACCGAGCAGCCAGGGGTCCACGTCCTGGGAGCCGTTGTAGGGCTGGTAGCGGAT
     <N  G  W  V  V  C  V  R  K  G  R  R  P  G  L  L  W  P  D  V  D  Q  S  G  N  Y  P  Q  Y  R  I
39516 CGGGATCCGCAGCGCGTCGCCCATCGGCGGGATCGCCACGTCGGGCGACGGGTCGATGGCGTACCGGATCTGGTGCCGGCTCCACTCGACGC
     <  P  I  R  L  A  D  G  M  P  P  I  A  V  D  P  S  P  D  I  A  Y  R  I  Q  H  R  S  W  E  V  G
39608 CGTACTTGCGGAACTCGGTCACCGGGTCGCCGGAGACCAGGTCGAGCCCGGGCTCGGTCTCGATGGTGCCGATGAACCCGGGCGAGAAGTAG
     <  Y  K  R  F  E  T  V  P  D  G  S  V  L  D  L  G  P  E  T  E  I  T  G  I  F  G  P  S  F  Y
39700 ACGCTGGGGATGTGGTGCAGCTCGGCGACCAGCGCGCCCTCCACGGCCATGATGTCGTGGACCACCAGGTCGGGCCGGTAGTGGGCGGCGTA
     <V  S  P  I  H  H  L  E  A  V  L  A  G  E  V  A  M  I  D  H  V  V  L  D  P  R  Y  H  A  A  Y
39792 GTCGACCGCGTTGTCGTAGCTGCGCTGGACCGCGGTGACCGTGCGCTTCCAGTAGTCGGCGAGCAGGTCGGTGTCGAAGTCGGCGAGCGAGT
     <  D  V  A  N  D  Y  S  R  Q  V  A  T  V  T  R  K  W  Y  D  A  L  L  D  T  D  F  D  A  L  S  D
39884 CCATCGGCCGGCCCGTGAAGGGTTCAACGGCAGCGGTTGCTCCACCATGTGCTGCGGGGTGTAGAGGCCTGGACGTAGAAGCCCAGCCGG
     <  M  P  R  G  T  F  P  N  L  P  L  P  Q  E  V  M  H  Q  P  T  Y  L  A  Q  V  Y  F  G  L  R
39976 GCGCTCTCCATCATGTCGGGTCCGTCGAGCACCGAGACGGGCATCATGCCCGCCGCGGCCACGCCCCGGACCTGGGACGGCGAACAGGCGAC
     <A  S  E  M  M  D  P  G  D  L  V  S  V  P  M  M  G  A  A  A  V  G  R  V  Q  S  P  S  C  A  V
40068 CTTGACGTCGTGGCCGGCCGCCCGCAGCGCCCAGGCCAGCGGCACCATGCACATGTAGTGCCCGGCCCAGTTGGACACGGTGAACAGAACCT
     <  K  V  D  H  G  A  A  R  L  A  W  A  L  P  V  M  C  M  Y  H  G  A  W  N  S  V  T  F  L  V  K
40160 TCATCGCAGCCTCTCTGTGGCCTGCCGAGGGGAGGTTGGGGGTCGCGGCCGGACGGTCAGGAGGTCAGGACCGGCAACTCCCGCGCGGGA
     <  M                                                  <  o  S  T  L  V  P  L  E  R  A  P
40250 TCGGCGAACTCGATCACGATGGTGCGCCGCCACTGGTCGGAGGGGTTCGGCCCGGAGCCGTGCACCAGCCGTACGTCGTGGACGATGAAGTC
     <D  A  F  E  I  V  I  T  R  R  W  Q  D  S  P  N  P  G  S  G  H  V  L  R  V  D  H  V  I  F  D
40342 CCCCTCCTGCGAGGGGACCGGCACCCGCGGCCCGGCGTCGCGCACGGCCGTGACGTCGGCGTCGTCGGGCAGCAGGTGGGAGCCGGGCACGC
     <  G  E  Q  S  P  V  P  V  R  P  G  A  D  R  V  A  T  V  D  A  D  D  P  L  L  H  S  G  P  V  G
40434 CCTCCAGACAGCCGTTCTCCGGCCCGGCGGTGTCCAGGCAGATGCTGATGTTGCAGACCGCGTGCGGGGGGACGTTGACCCGGTCCCGGTGC
     <  E  L  C  G  N  E  P  G  A  T  D  L  C  I  S  I  N  C  V  A  H  P  P  V  N  V  R  D  R  H
40526 CACGGCACGCCGGCCGCCCGCAGTGGCTCCTTGAGCACCAACGCGAAGGCGGTGGGCACGACCGGGGTGCCGAGGACGTCGGCGGCCACCGC
     <W  P  V  G  A  A  R  L  P  E  K  L  V  L  A  F  A  T  P  V  V  P  T  G  L  V  D  A  A  V  A
40618 GGCGATCTCCGGCCGGTGCAGCAACTCGCCCTGCGGCCAGTCCTGCTTTTCGAGGTTGTGGATCCGGTACAGCACCGGCTCCGCGCCCTCGA
     <  A  I  E  P  R  H  L  L  E  G  Q  P  W  D  Q  K  E  L  N  H  I  R  Y  L  V  P  E  A  G  E  V
40710 CCTCGTAGTTCCAGTAGTCGGCGTTGGCCCGCGCCGGACCGGCGAACCGGTCGATCAGGCTTACCGCGCCGGCCTTGAGCTGGGCCAGCACC
     <  E  Y  N  W  Y  D  A  N  A  R  A  P  G  A  F  R  D  I  L  S  V  A  G  A  K  L  Q  A  L  V
```

Figure 11K

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40802 TCGGGGTCGAGCACCGGCCCGACGTGCGCGATCCCGTCGCTGCGGAACCGGCTGGCCACGGCCTCGCGCTCCCGCGACATGGTGGTCATCG
     <E  P  D  L  V  P  G  V  H  A  I  G  D  S  R  F  R  S  A  V  A  E  R  E  R  S  M  T  T  M
                                                                                          <  o  R
40893 GAGGCTCACCCCTTCGGTCGGTCGGCGCGTGCCGGTGCGGCGGCCGACGGCGATGATGTCGCACACCTCCGGCGACCGGCGCTCGTGCAGC
     <  L  S  V  G  E  T  P  R  R  T  G  T  R  R  G  V  A  I  I  D  C  V  E  P  S  R  R  E  H  L
40984 ACCTCCACCTCGGCGAAGCCGGCGTTGTGCAGGGCGGCGAACAGGGACTCCCGGTCGAGCCAGCGCACGTCGACGCTGAGCCCCCGGGCCTG
     <V  E  V  E  A  F  G  A  N  H  L  A  A  F  L  S  E  R  D  L  W  R  V  D  V  S  L  G  R  A  Q
41076 CGGCTCGGGGTGCTCCTCGCGGACCTGCTTGACCGTGTAGCCGTCGATCGGTTGCAGGTCGCCCACGCCTCCCCAGTAGTGGGTGGAGAGGT
     <  P  E  P  H  E  E  R  V  Q  K  V  T  Y  G  D  I  P  Q  L  D  G  V  G  G  W  Y  H  T  S  L  Y
41168 AGATTCCCGCCGCGACGCCCGCGATGTCCTTCAGCAGGGTCCACGGCTCACGCACGTGGTAGAGCAGGCCCGCGCAGAGGACGGCGTCGAAC
     <  I  G  A  A  V  G  A  I  D  K  L  L  T  W  P  E  R  V  H  Y  L  L  G  A  C  L  V  A  D  F
41260 TCGCCCAGCTCGGTGAAGTCGATCCGCTCCACGTCGGCGACGCGCAGCTCCACGTTGGTGATGCCGTTGACCTCCATCACCAGCTCCGCGCG
     <E  G  L  E  T  F  D  I  R  E  V  D  A  V  R  L  E  V  N  T  I  G  N  V  E  M  V  L  E  A  R
41352 GCGCAGGTTCTCCGGACGGCCCTCCAGGGCAAGCACCGTCGTGCCGGGGTGCCGGGCGAGGGCAAGCGTGTCCGCGCCCTCCAGTGCGCCGA
     <  R  L  N  E  P  R  G  E  L  A  L  V  T  T  G  P  H  R  A  L  A  L  T  D  A  G  E  L  A  G  L
41444 GTTCGAGGATCCGCCGCGCGTCGGGAAACGCACCGAAGAACTTCGCGGCCCGGTCGGCCGGGGACTGGCTCAGCAGATAACCGTGCTGGGAG
     <  E  L  I  R  R  A  D  P  F  A  G  F  F  K  A  A  R  D  A  P  S  Q  S  L  L  Y  G  H  Q  S
41536 CCCTCGGCGTAACGCACTCCGTCGTGCTCGAATCCATTCACCCACGGCTCGAGCGCGGCGACGCGGCGACGAATCTCTTCACGGTCCATGG
     <G  E  A  Y  R  V  G  D  H  E  F  G  N  V
41627 GATCAAAGCCTAGCGATGCCATTGCGGTTGCGGACTAGTGTTTTCATCATATTCAGCGGCTCGCCGTGCTGAGCCTTTCGTTGACCAGCCG
                                                                                <  o  R  S  A  T  S  L  R  E  N  V  L  R
41718 GGCCCATTCCGGAATCCGGTCCCCGCCGATCTCGATATCGAAGGACGACTGGAGTTCCGCCGGCCCGGCGTCGGCCGCCCACCTGGCGGTGC
     <  A  W  E  P  I  R  D  G  G  I  E  I  D  F  S  S  Q  L  E  A  P  G  A  D  A  A  W  R  A  T  R
41810 GGGCCAGTCCCTCGGCCAGCGGGGTGTCCGTCCAGTCGCCGAAGACCGATCGGGCCAGCTCCGTCGCGGTGTACGCGGTTCGCACCTCGTCC
     <  A  L  G  E  A  L  P  T  D  T  W  D  G  F  V  S  R  A  L  E  T  A  T  Y  A  T  R  V  E  D
41902 CGCGACGGCAGGTGGGCGATCGGATGCTCCGGCACGCCGGCCGCCGACCGTACCGCCTGGGCCAGCTCCAGCACGGTGTTGGTGCTCGACGA
     <R  S  P  L  H  A  I  P  H  E  P  V  G  A  A  S  R  V  A  Q  A  L  E  L  V  T  N  T  S  S  S
41994 GCCCACGTTGAATGCCCGCCCCCACGCGGCCTCGGTCTCGGCGGCGCGGCTGACCACGTTCACCACGTCACCGACGTACGTGAACGCGCGGA
     <  G  V  N  F  A  R  G  W  A  A  E  T  E  A  A  R  S  V  V  N  V  V  D  G  V  Y  T  F  A  R  V
42086 CCTGGCCGCCGTCGCCGTACACGGTGATCGGCTCGCCTCGCAGGATCTGGTTGAAGAAGATGGCGACCGCGTTGCGGTACGGGTCCCGCATG
     <  Q  G  G  D  G  Y  V  T  I  P  E  G  R  L  I  Q  N  F  F  I  A  V  A  N  R  Y  P  D  R  M
42178 TTCTGCCACTCGCCGTAGACGTTGTGCATGCGGAAGGCGGTGAAGGGCAGCCCCTGGGTCCGCATCGTCACCTCCAGCTCGCGCTCGACCAG
     <N  Q  W  E  G  Y  V  N  H  M  R  F  A  T  F  P  L  G  Q  T  R  M  T  V  E  L  E  R  E  V  L
42270 GTACTTGGCCAGGCCGTAGCTGTCCGCGGGGACGGGGACGACGGACTCGCGCATCGGCGTCTCGCCGTGGCCGTAGACCGCCACGGAGGAGG
     <  Y  K  A  L  G  Y  S  D  A  P  V  P  V  V  S  E  R  M  P  T  E  G  H  G  Y  V  A  V  S  S  A
42362 CGAAACAGAAGAACCGCACGCCGGTACGCAGCGACGCGTTGATCAGATTTATGCTGCCCATCACATTGGTGCCGTAGTTGAGCTGCTTCACC
     <  F  C  F  F  R  V  G  T  R  L  S  A  N  I  L  N  I  S  G  M  V  N  T  G  Y  N  L  Q  K  V
42454 GAATGGCTGATCGCCTCCGCCGCGAAGGCGGCAAAGTGGAAGACCCGCTCGAATCGGTTCTCGGCGAACAGTGAATCGACGAAGTCCACGTC
     <S  H  S  I  A  E  A  A  F  A  A  F  H  F  V  R  E  F  R  N  E  A  F  L  S  D  V  F  D  V  D
42546 GGTCACCGAACCGACGGCCAGGTCCACCCCGGCCGGAACCCGCTGCCGGCTGCCGCCGCTGAGGTCGTCCAGAACGGTGACCCGGTGCCCAT
     <  T  V  S  G  V  A  L  D  V  G  A  P  V  R  Q  R  S  G  G  S  L  D  D  L  V  T  V  R  H  G  N
42638 TCCTGACCAATGACTCCACCAGGTGCGAGCCGATGAATCCGGCACCACCAGTCACCAGACAACGAACCATCCGGGGCTCCTTCGTCAATA
     <  R  V  L  S  E  V  L  H  S  G  I  F  G  A  G  G  T  V  L  C  R  V  M
42728 GATCCGGAAAGGGTTGACCGAGCGGGCGATCTGCGGCGCGCCCTTCGTCGGCGAACACCGACCCCCGAGAGAAAGCTTCGCCTCAGGGCAC
                                                                                          <  o  P  V
42819 CGGCGACCGGTCGGCCTGCTTCTTCAGCGGCTCCCACCAGTCCCGGTGCGTCCGGTACCAGTCGATCGTCTCGGCCAGGCCGTCGGCGAAGG
     <  P  S  R  D  A  Q  K  K  L  P  E  W  W  D  R  H  T  R  Y  W  D  I  T  E  A  L  G  D  A  F  A
42911 CGACCTCGGGCCGGTAGCCGAGCGCCCGCAGTTTCGCGTCCGTCAGCGAGTAGCGGCGGTCGTGGCCCTTGCGGTCCGGCACCCGCTCGACC
     <  V  E  P  R  Y  G  L  A  R  L  K  A  D  T  L  S  Y  R  R  D  H  G  K  R  D  P  V  R  E  V
43003 CGGTCCCACCCGGCCCCCAAGGCGTCCAGCAGCCGCCCGGTCAGCTCCATGTTGGACAGCTCAGCCGTGCCGGCGATGTGGTAGACCTCGCC
     <R  D  W  G  A  G  L  A  D  L  L  R  G  T  L  E  M  N  S  L  E  A  T  G  A  I  H  Y  V  E  G
43095 GGGGACACCGCGGTCGACGACGGTCTGGATGCCCCGGCAGTGGTCCGTCACGTGGATCCAGTCGCGGACGTTCCCGCCGTCGCCGTACAGCG
     <  P  V  G  R  D  V  V  T  Q  I  G  R  C  H  D  T  V  H  I  W  D  R  V  N  G  G  D  G  Y  L  P
43187 GCACCCGTCGCCCGTTCAACAGCTCGGTGACGAACAGCGGGATCAGCTTCTCCGGAAACTGGTACGGCCCGTAGTTGTTGCCGCACCGGGTG
     <  V  R  R  G  N  L  L  E  T  V  F  L  P  I  L  K  E  P  F  Q  Y  P  G  Y  N  N  G  C  R  T
43279 AGGCAGACCGGCAGCCCGTGGGTGCGGGCGTAGGCCAGGGCGATCAGGTCCCCGCCGGCCTTCGCCGCCGCGTACGGGGAGTTCGGCGCCAG
     <L  C  V  P  L  G  H  T  R  A  Y  A  L  A  I  L  D  G  G  A  K  A  A  A  Y  P  S  N  P  A  L
43371 GGGGGTGTCCTCGGCCCAGGAACCCTCGTCGATGCTGCCGTAGACCTCGTCGGTGGAGACCTGGACCACCCGGGCGACCCCGGCGTCGAGAC
     <  P  T  D  E  A  W  S  G  E  D  I  S  G  Y  V  E  D  T  S  V  Q  V  V  R  A  V  G  A  D  L  C
43463 ACGCCTGCATGAGCGTCTGGACGCCCTGCACGTTGGTGCGGACGAACTCCGCCGAGTCGGCGATGGACCGGTCGACGTGCGACTCGGCGGCG
     <  A  Q  M  L  T  Q  V  G  Q  V  N  T  R  V  F  E  A  S  D  A  I  S  R  D  V  H  S  E  A  A
43555 AAGTTGACCACCACGTCGTGCCCGGGCAGCACCTCGGCCAGCAGCGCCGTGTCGCAGACGTCGCCCTGGACGAAGGTGATCCGGTCCTGGAC
     <F  N  V  V  V  D  H  G  P  L  V  E  A  L  L  A  T  D  C  V  D  G  Q  V  F  T  I  R  D  Q  V
43647 CGGTTCGAGGTTGGCGAGGTTGCCCGCGTACGTCAGCTTGTCCAGCACCGTCACCCGGGCCTGCGCCGTGTCGGGGTAGGCACCGGTGGCCA
     <  P  E  L  N  A  L  N  G  A  Y  T  L  K  D  L  V  T  V  R  A  Q  A  T  D  P  Y  A  G  T  A  L
43739 GGTCGCGGACGTACTGCGAGCCGATGAAACCGGCACCGCCGGTGACCAGGACGCGACGCATCAGACCCCCACCCGGACTTCGCTGTGAT
     <  D  R  V  Y  Q  S  G  I  F  G  A  G  G  T  V  L  V  R  R  M
                                                                                <  o  V  G  V  R  V  E  S  H  D
43828 CGCCGAGGACGAACCGGTGCGTCTTGGGCACCCGGGGCCCGGGGACCACCCGCGCCTCCCGGCCGATCATCGAGAACTCGATGCGGCCGATG
     <  G  L  V  F  R  H  T  K  P  V  R  P  G  P  V  V  R  A  E  R  G  I  M  S  F  E  I  R  G  I
43920 CCCTCGATGTAGGCACCGCGCAGCACGATGGAGTGCTCGATCTCGGTCTCCAGCAGGGTGCAGTCGCAGTCGATCGAGGTGTACGGGCCGAG
     <G  E  I  Y  A  G  R  L  V  I  S  H  E  I  E  T  E  L  L  T  C  D  C  D  I  S  T  Y  P  G  L
44012 GTAGGAGTTGCGGATGATCGAGCCGGCTCCGACCACCACCGGGCCGACGATCCGGGAGCCGCTGACGTCGGCGCCGGCGCTGATCACCACCG
     <  Y  S  N  R  I  I  S  G  A  G  V  V  V  P  G  V  I  R  S  G  S  V  D  A  G  A  S  I  V  V  P
44104 GGCCGATCAGTTCGGTGCGGTCGTCGACCTTGCCCTCGACCAAAGGCTCGACGCTGCCGAGGACGAACCGGTTCATCTCCAGCATGTCGGCG
     <  G  I  L  E  T  R  D  D  V  K  G  E  V  L  P  E  V  S  G  L  V  F  R  N  M  E  L  M  D  A
44196 AGGTTGCCGGTGTCCTTCCAGTAGCCCGTGATCATGGTGGAGTCGACCCGGTGGCCGCGGTCGATCATCCACTGCACCGCGTCGGTGATCTC
     <L  N  G  T  D  K  W  Y  G  T  I  M  T  S  D  V  R  H  G  R  D  I  M  W  Q  V  A  D  T  I  E
```

Figure 11L

```
44288 CAGCTCGTTGCGCCAGGACGGCTTCAGCTCGGCCACGGCATCGTGGACCACCGGGCTGAAGACGTAGACCCCGACCAGGGCCAGGTCGCTCT
      < L  E  N  R  W  S  P  K  L  E  A  V  A  D  H  V  V  P  S  F  V  Y  V  G  V  L  A  L  D  S  K
44380 TGGGGTGCTCGGGCTTCTCCTCCACCCCGATCACCCGGCCGTCCGCGCCCATCTCGGCGACGCCGAAGGCGTGCGGGTCGGCGACCCGGGTC
      < P  H  E  P  K  E  E  V  G  I  V  R  G  D  A  G  M  E  A  V  G  F  A  H  P  D  A  V  R  T
44472 AGCATGATCTGCGCGTGCGGTCGCTCCTGCCGGAAGCGCTCGACGATGTCCTTGATCCCGCCGACGATGAAGTTGTCGCCGAGGTACATGAC
      <L  M  I  Q  A  H  P  R  E  Q  R  F  R  E  V  I  D  K  I  G  G  V  I  F  N  D  G  L  Y  M  V
44564 GAAGTCGTCGTCGCCGAGGTAGTCGCGGGAGATGAGCACGGCGTGCGCCAGCCCCCGGGGAGCCTCCTGCGGAAGGTAGGTCACCTGGAGGC
      < F  D  D  D  G  L  Y  D  R  S  I  L  V  A  H  A  L  G  R  P  A  E  Q  P  L  Y  T  V  Q  L  G
44656 CGAACTGGGAACCATCGCCGACCACGCGCTGAATTTCGGGCGCGGTGCTGCCGACGACGATGCCCACCTCCTCGATACCGCCCTCACGAATA
      < F  Q  S  G  D  G  V  V  R  Q  I  E  P  A  T  S  G  V  V  I  G  V  E  E  I  G  G  E  R  I
44748 GCCTCGAGCCCGTAGAACAGCACCGGCTTGTTGGCCACGGGAATGAGTTGTTTGGCGGACGTGTGGGTGATCGGACGCAATCTCGATCCCAC
      <A  E  L  G  Y  F  L  V  P  K  N  A  V  P  I  L  Q  K  A  S  T  H  T  I  P  R  L  R  S  G  V
44840 CCCTCCCGCCAGGACCAGCGCCTTCACGAACGCCCTCGAAAGGATGGGACCGAGACGGGTCGCTGGTTCACGAGCACTCCAGGGGTCACGG
      < G  G  A  L  V  L  A  K  V
44931 TGGACTGGGCTCTTCGTGAACGTACCGAAGGATCACTCGTGATTTCCCTACTTATGGGCCACCGAGGTGTGATCGGTGGATCTCTATGCGT
                                                                                  <  •  A  D
45022 CCGCCATTTCCGCAAACGGGGGCCTGGCCGGCCCGCCGCCGACCAGTTCGAGCACGGCGGCCAGGCCGTGCACGGTGTCCGGCGGGCTGGCC
      < A  M  E  A  F  P  P  R  A  P  G  G  G  V  L  E  L  V  A  A  L  G  H  V  T  D  P  P  S  A
45114 GGCAGCAGCAGGGTCTGCAGGCCGGCGTACACCGCCCCACCGTCGGCCAGGGTGTCGCCCACCATCAGCGCCCGCTCCGGGGCGACCTTCAG
      <P  L  L  L  T  Q  L  G  A  Y  V  A  G  G  D  A  L  T  D  G  V  M  L  A  R  E  P  A  V  K  L
45206 CTCGTCGCAGGCGGTGCGGAAGATCCGGGGATCGGGCTTGACCGCCCCCACCTCGTGGGAGAAGACGTAGGCGTCCACCAGCTCCGCCATCC
      < E  D  C  A  T  R  F  I  R  P  D  P  K  V  A  G  V  E  H  S  F  V  Y  A  D  V  L  E  A  M  G
45298 CGTACGCCGCGAAGGTGGGCCGCAGGTCCCAGGCGATGTTGCTGACCACGGCGGTGCCCACGCCGCGCCGGCGCAACTCCGCCAGGACCGGG
      < Y  A  A  F  T  P  R  L  D  W  A  I  N  S  V  V  A  T  G  V  G  R  R  R  L  E  A  L  V  P
45390 GCGGCGTCGCGGTAGGGCAGCCAGCCGTCCGTGCGGAACAGCCGGTCGTAGAGCGCCTCGGCGAGGCCGGGATGGGGCAGGTCGACGGTGGA
      <A  A  D  R  Y  P  L  W  G  D  T  R  F  L  R  D  Y  L  A  E  A  L  G  P  H  P  L  D  V  T  S
45482 GAGCAGGCCCACGTACGCGCTGCGGTGCGTTTCGGGCGAGAGGTCCCGGCGGGCGTACACCTCGGCGAGCCCCGGCGGGACGGCGTGCGGCT
      < L  L  G  V  Y  A  S  R  H  T  E  P  S  L  D  R  R  A  Y  V  E  A  L  G  P  P  V  A  H  P  E
45574 CCGGCCCGCCGGGACGGCCGGCCGCCAGCAGCAACCCGGTCAGGGCCTCCTGCTGCGCCGGGTCGAGCTGGACGCCGACGGTGGCCGCCGCC
      < P  G  G  P  R  G  A  A  L  L  L  G  T  L  A  E  Q  Q  A  P  D  L  Q  V  G  V  T  A  A  A
45666 GCCCGCAGCCAACGCTGCGGCAGTTCCACGGCGAACAGCGTGCCGGAGAAGTCGAACAGGACGGCGTCGATCGGACGGGGCAGGGGGGTCGT
      <A  R  L  W  R  Q  P  L  E  V  A  F  L  T  G  S  F  D  F  L  V  A  D  I  P  R  P  L  P  T  T
45758 CATCGCTCTCCTCGGTGCAGCCGCGTCAGGGCGGCACCAGCCTGGCAGCGGACCAGCCGGATGTCCATCATGGAGGAATGCGCCGGGTCG
      < M
45848 GGCGCGCCCGCCATGGCCGCCGGTCCGGACGACAGGCATTTTCGGTCACTCTTGCCTTCTAGGCGGATTTCTTCAAAGATGGCTGTCAATTC
45940 TTCAGCGATCCTGGAGGCATCCGTGACCCGTACCCGAACCGCCCTGCGCCGGCTGCTCGCCGCCGGTCTGGCCAGCCTCGCCACCGCTGC
                            > V  T  R  T  R  T  A  L  R  R  L  L  A  A  G  L  A  S  L  A  T  A  A
46030 CGCGACCCTCGTCGCCACCGCCGGCCGGCGGCGGCCGCCACCACCCCCGGCATCGACGTGTCCCACTACCAGGGATCGATCAACTGGACGA
      > A  T  L  V  A  T  A  G  P  A  A  A  A  T  T  P  G  I  D  V  S  H  Y  Q  G  S  I  N  W  T
46122 GCGTCCGCAACGCGGGCATCCAGTTCGCGTTCATCAAGGCCACCGAGGGTACGAGCTACAAGGACCCCAACTTCAACGCCAACTACGTCAAC
      >S  V  R  N  A  G  I  Q  F  A  F  I  K  A  T  E  G  T  S  Y  K  D  P  N  F  N  A  N  Y  V  N
46214 TCCTACAACGCCGGAGTGATCCGGGGGGCGTACCACTTCGCCCGGCCGAACATCTCCTCCGGCGCCACCCAGGCCAACTACCTGGCCAGCAA
      > S  Y  N  A  G  V  I  R  G  A  Y  H  F  A  R  P  N  I  S  S  G  A  T  Q  A  N  Y  L  A  S  N
46306 CGGCGGCGCCTGGTCGGCGGACAGTCGCACCCTGCCGGCCGCGCTGGACGTCGAGGCCAACCCGTACAGCGGCGGCACGTGCTACGGCCTCA
      > G  G  A  W  S  A  D  S  R  T  L  P  A  A  L  D  V  E  A  N  P  Y  S  G  G  T  C  Y  G  L
46398 GCACGTCCGGGATGCGTAGCTGGATCCAGGACTTCCTGAACACGTACAAGGCCCGCACCGGCCGGTACGCGGTCATCTACACCACCACGAGC
      >S  T  S  G  M  R  S  W  I  Q  D  F  L  N  T  Y  K  A  R  T  G  R  Y  A  V  I  Y  T  T  T  S
46490 TGGTGGAACCAGTGCACCGGTAGCTGGACCGGGCCGTGGGCCAACCACCCGCTGTGGCTCGCCCGCTGGTCGAGCACCCCGGGCACCCTGCC
      > W  W  N  Q  C  T  G  S  W  T  G  P  W  A  N  H  P  L  W  L  A  R  W  S  S  T  P  G  T  L  P
46582 GGCCGGCGCTTCGGTCTGGAGCTTCTGGCAGTACACGGCCTCCGGCAGCGTCTCCGGGATCAGCGGCAACGTCGACCGCAACAACTGGAACG
      > A  G  A  S  V  W  S  F  W  Q  Y  T  A  S  G  S  V  S  G  I  S  G  N  V  D  R  N  N  W  N
46674 GCGACCGCACCCGGCTGATCGCGCTGGCGAACAACACCTGACCCGAACGCCCGGGTAGGCGGTTGGCGGCAGCGGAACCGATTGCGACCGT
      >G  D  R  T  R  L  I  A  L  A  N  N  T  •
46765 ACGGTCGGCGGCCGGTCCGGCTGCCGCCAGCCCGTCACCCGGCCCGCGTCGCGGGCCGCGCCGGCATCCGGTCCTGCCGGCCCGGGGTGGCC
46857 CGCCGTGCCATCCGCCAGGCGGCCACGCCTGCGACGGCGCCGGCCACGACACCGAACAGCGCGAACAGCACCGGAAGACCCGCGCTGACCAG
46949 CAGCAGCACCACGTCGCCGAAGGCGACGAGCATCCACAGTGCCAGCCCGGGTCGAGCGTCCCTGCGTCGGTGTCCCATGTCGCACCTCCTCG
47041 CATCGTCCGGGATCAGATACCCCGTTCGACGCAAGTACATGCGAATCGACATCGCAACGGCGGGAATCGCCTGCTCAGCGGGCCGAGTCGGC
47133 AATGGACGGCCCCGGCCGGGCGCTCAGTCGACCCGGTCCGGCTTGAAGCCCTTGGCGATCCGGTCGAAGTCGGCCAGCCGCGCCTGCCAGT
                                  <  •  D  V  R  D  P  K  F  G  K  A  I  R  D  F  D  A  L  R  A  Q  W  D
47224 CCTTGTTCGCCACCTCCCACCGGAGGGCGTACCCCCGGTTGCTGGCCGTGACGAAGCCCCGGTTGCGGACGTGGATCCGAGTGCCGTCCCGG
      < K  N  A  V  E  W  R  L  A  Y  G  R  N  S  A  T  V  F  G  R  N  R  V  H  I  R  T  G  D  R
47316 TTCTCCAACCACTCCCAGTCCGCGCACGTCTTGTAGTAGTCGCAGCGCTTGATGCTCAGATACTGGTAGCCGTTGACGTAGTTCTTCCGGGC
      <N  E  L  W  E  W  D  A  C  T  K  Y  Y  D  C  R  K  I  S  L  Y  Q  Y  G  N  V  Y  N  K  R  A
47408 CGGTTCCTTCTCTTTCCAGTCGGCGTAGGCGTCGCCCTCCGGGGTGCTGGTCCACTGCACCAGCAGCTCGCCCACCCCGTCGCGCTCGTCGA
      < P  E  K  E  K  W  D  A  Y  A  D  G  E  P  T  S  T  W  Q  V  L  L  E  G  V  G  D  R  E  D  F
47500 AGACGATCGTGTTCTGCCCCACGCTGCGCCGCACCCAGCCCTTCGGCAGGGGCAGCGAGAAGCCCGCCGGGTCCTTGTGCAGGAGCCAACCC
      < V  I  T  N  Q  G  V  S  R  R  V  W  G  K  P  L  P  L  S  F  G  A  P  D  K  H  L  L  W  G
47592 TCGGGCAGGGCGTTCGGGTCCACGGACGGGCTGGCAGACGGCGTCGGGCTGGGCGGAGCCGCGCTGCTGGTCGCCGGTGCGGCCGACGGCGT
      <E  P  L  A  N  P  D  V  S  P  S  A  S  P  T  P  S  P  P  A  A  S  S  T  A  P  A  A  S  P  T
47684 CGGCGTCGACACGCCCGCCTGCGGGTCGCCGCCGGGCCCCGGGTCGTCGTCACCGCTCCGGCCGAGCAGCGGCACCGCCGCCAGCAGGCCGA
      < P  T  S  V  G  A  Q  P  D  G  G  P  G  P  D  D  D  G  S  R  G  L  L  P  V  A  A  L  L  G  I
47776 TCAGCAGCACCGCGACGAGCGCGCCGACCAGCAGGCCGCGGCGGCGACGCTCGGGCTTCGTGCCCCCGACGACGGTGGCCCGGCCCGTCGAC
      < L  L  V  A  V  L  A  G  V  L  L  G  R  R  R  R  E  P  K  T  G  G  V  V  T  A  R  G  T  S
47868 GAGAGTGCCGGGCCGGAGGCGGCCGGCAGCACCGACGTCGGGGCGGCCTCCTCGCGGGGCGCGACGGCGGGCTCGCGGGCCGGGGCGGGCGG
      <S  L  A  P  G  S  A  A  P  L  V  S  T  P  A  A  E  E  R  P  A  V  A  P  E  R  A  P  A  P  P
47960 CGAAACGGGCACAGCCGCGCCCGGATCGACCCGGGTGTCGTCGGCTCGGGTGTCGTCGGCCCGACCGGCCGCCGGGGCCCCGTCGGCCCCTT
      < S  V  P  V  A  A  G  P  D  V  R  T  D  D  A  R  T  D  D  A  R  G  A  A  P  A  G  D  A  G  E
48052 CGTCCCCAGCCTCGGCGGCCCGGTCCGCCGGCGGCCCGTCACTCCCTCCGGCCGGCGTGCCCGCAGCCTCGTCGGCGCTGGTCGCGGCGTCG
      < D  G  A  E  A  A  R  D  A  P  P  G  D  S  G  G  A  P  T  G  A  A  E  D  A  S  T  A  A  D
```

Figure 11M

```
48144 GGGGCGGGGATCTTCGCGGTGGGATCGGCCGCCTGCGGGCCGAAGTCGGTGACCTTCGCGGTCGGATCGGCGTCGGCGCTCGGCAGGTCGAC
     <P  A  P  I  K  A  T  P  D  A  A  Q  P  G  F  D  T  V  K  A  T  P  D  A  D  A  S  P  L  D  V
48236 CATCGCGGTCGGCGCGGCGTCCACCCCCGCCGGGACCTTCGCGGTCGCGTCGCCGCCGCCCACGCCGGCCGCCGCCGCGCCACCGGCGGCAA
     <  M  A  T  P  A  A  D  V  G  A  P  V  K  A  T  A  D  G  G  G  V  G  A  A  A  A  G  G  A  A  L
48328 GACCACCTTCCGGGGTACGCGGTGCGGGCGGGGCCGCCGGCCGGCCGGTGCGCTGTTCGGCGGGGCGCGGTGCGGGCACCACCGGCGGTCGC
     <  G  G  E  P  T  R  P  A  P  P  A  A  P  R  G  T  R  Q  E  A  P  R  P  A  P  V  V  P  P  R
48420 GGCTCGCGCGGGCCGTTCGGCCCCGGCCGGCGTACGCCGTCGAGCAGCGAGATGGTCTTGGCGCGACGCCCGGCGGCCCGCCGCAGGAGCCG
     <P  E  R  P  G  N  P  G  P  R  R  V  G  D  L  L  S  I  T  K  A  R  R  G  A  A  R  R  L  L  R
48512 CTCGGCCACCTCGGCGTCGATCCGCTCGGCCGGGTCCTTGCGGAGCAGCCCGTTCAGCACCGGCTTCAACGGGCCGGCGTTCCTCGGCGGCG
     <  E  A  V  E  A  D  I  R  E  A  P  D  K  R  L  L  G  N  L  V  P  K  L  P  G  A  N  R  P  P  P
48604 GCATCGGCTCGGTGGCCAGCGCCGCCAGGGTGGCGATCGCCGACGGTCGGGCGAACGGCGACTTGCCCTCCACCGCCGCGTAGAGCGTCGCG
     <  M  P  E  T  A  L  A  A  L  T  A  I  A  S  P  R  A  F  P  S  K  G  E  V  A  A  Y  L  T  A
48696 CCCAGCGACCAGAGGTCCGCCTCCGGGCCGGCGGTGCCGTCCCGCGCCCGCTCCGGGGCGATGTACGCCGGGGAGCCCAGCACCATTCCGGT
     <G  L  S  W  L  D  A  E  P  G  A  T  G  D  R  A  R  E  P  A  I  Y  A  P  S  G  L  V  M  G  T
48788 CCGCGTCACGTTCGGGTCACCGGGGATGGTCGCCAGGCCGAAATCGGTCAGCACCACCCGGCCGTCGGTGCCGAGCAGCACGTTGCCCGGCT
     <  R  T  V  N  P  D  G  P  I  T  A  L  G  F  D  T  L  V  V  R  G  D  T  G  L  L  V  N  G  P  K
48880 TGATGTCCCGGTGCATGACGCCGGCCTTGTGCGCCGCCTTCAGCGCGCCGAGCACCCCCAGGCCGATCTCGACCGCCTTGGCCGGCGACACC
     <  I  D  R  H  M  V  G  A  K  H  A  A  K  L  A  G  L  V  G  L  G  I  E  V  A  K  A  P  S  V
48972 GGCCCGTCCTCCGCGAGAGTGTCCTGAAGGGACTTCGACGCCACGTACTCCATGACGATCCACGGGTCGCCGTCGGTGCGCAGAACGTCGAA
     <P  G  D  E  A  L  T  D  Q  L  S  K  S  A  V  Y  E  M  V  I  W  P  D  G  D  T  R  L  V  D  F
49064 GATGCGGACCACGTTGACGTGGTTGAGTCGCGCGATGGCACGGGCCTCCCGCAGCGAGCGTTCCCGCATCTCGCGGCGCTCCTCCGGGGTGA
     <  I  R  V  V  N  V  H  N  L  R  A  I  A  R  A  E  R  L  S  R  E  R  M  E  R  R  E  E  P  T  L
49156 GGCTGGGCGGCGGGACCAGTTCCTTGATCGCCACATCCCGGTGCAGCACCTCGTCGCGCGCCTTCCATACCCGACCCATGCCACCCTGACC
     <  S  P  P  P  V  L  E  K  I  A  V  D  R  H  L  V  E  D  R  A  K  W  V  R  G  M
49247 GAGCGGCGAAATCAGCCGGTACCGGTCGGCAACGAGTTGGGGAAGCGCGTTCGACATCGGTGGAGACGGTACCCGGCGGCGGCCCGCCGCAC
49339 ACCGCCGGCACGCCACTGTGCGACGAAGGTCAAGTTCGCGACGCGTACGCTGAACGGCATGTCTGCCGAAGAGCCGCTGTTCCGGGTGACCC
49431 GGGGCGTTCCGACCGCCGAGGAACTGGCCGCGCTGGTCGGCGTCATCGTCGCCCGGACCCGCTCCGCCGCCGCTCACGCGCCCGCCGCGCCG
49523 TCGGCCTGGGCACGCAGCGGTCGGCCCGGCGGTACGGTGCTCGCCGCTCGCCCGGGAGCCTGGCGCGCCTCCGGTCTGCCCCGCTGACGCAC
49615 TCGCCAGCATGTGGCCAGTGTGGCCCGCCGCCGAGGCGGGTGGCGGCGGGGGCTCCCGGAGGTCGACGACACCCGTTAACCTCACTCAGGGA
49707 GACGATGCCGTGACGGATAGGGAGGGTCGATGATTCCCGAGGAGGACCGACCAGCACCCTGGTTGAGCGGCTACGGCAGCATCGAGGCCGAC
49799 ATCCGCCAGATGCGCGAGTTCGCCGACAAACTCCAGGCGGAGGTCGAGCGGAACTACGCACCGCATCTGTCGTACATAGCGGACGACATGAA
49891 GGCACAGATCCCCAACCCCGCCGACGCCTTCGTCGAACTGGTGCAGTTCCTCAAGGCGCACAACGAGACCCAGCAGGCCACCGCCACGATGG
49983 TCTGGTCCGTCGGTGGGGCCACCGGCCACCTGGCCACGGCAGCCGGCCGGATCGCCGAGCAGTACGCCGACTCCGACGCCTTCTCCGCCGCT
50075 CGCGTCTCCGACGTGGAGCGGGCCCTCGCCAACCCGGGCGCGGCGGGGCAGGGCCGCCCCACGCCGGCTCTGCCCGACCCGACCAGCCCGGA
50167 CGGCGGGCCGGGGCGGGTGGTGCTGCCATGATCGAGCGGGGCAGCGGCCGGACGTCCGGCCTCACCGACTGGCGGCTGATGGACCTGCTGAG
50259 CATGTGGGCGTGCATCCAGGACCACGAGACCGCCGGGCACTGGAAGCAGGTCGCCGGCTGGCGCAAGGTTTGCGACCTCGCGCAGGCCCACC
50351 TGGGCCGCCTCAAGGAGTACCGGCGCGGCCTGGCCGAGGCGTGGCCACCGGCGACCAACGCCGCCGCCCGGGCGTACCTCGGCGAACTGGAC
50443 GACCTGATCGACAAGGTGCAACGCACCCACGACGCGGCTGCCGCGAACTACGACGCCCTCGCGGCCGCCACCCGAGCGATCAGCAGCGCCCG
50535 CACCGAACTCAAGCCGCTACACGACGAGTACGTGGAGAAACTCCAGCAGAAGCGGGCGTACGAGGCGACTACCGCCGATCCGAAGGCGCTGA
50627 TGGGCAGCCGGCTGCCGGACAAGCCGGTGACTGACGCCGACCTGGAACGACTCAACGCCCAGGCCCGGAACCTGATGTACGGGTTGAGCGGC
50719 GAACTCCAACAGGCCCAAGCAATGCTCCGCCAACCCCCTCCTCCGCACCGCCCAGGACGACAGCCGAACAACCCGGATGCTTACGAGAGCAC
50811 AGGCACGCCTCCGGTCATCCCGCCCGTATTACCAGTCCCAACCATTAGGCCTTCAATTCCCTCAAGCGCTCAGCAAGCAGAGCCACGCCCTG
50903 TTCCTGTCCAGAGCGCACCCCAAACAGGTCCTGTACTCGGGGGAATCGGGACGGGAAACACCACTTCGCCATCGGGCTCCATTTCTCCCGGC
50995 ACCGGCCACCCAGTGACATCCAACCCGGCAGGAGGTGCTGGCCCTACCCTCCCGCCGAACTTGCCACCTGCCATCGCCCCCACTGGACGAGG
                                                                                  junction marker
51087 CAGCACAACCGGCCAGGTAGGAAACCAGCCCCGCTCAACCACGTCCTCACGACCATTCTTGCCAGGCGGCCTGATCGGCGGCGGGCCCGCGA
51179 TGGGGATTAATCAACCCCTTGGCAATACTCCTCCGCGAAGGATCAACCCAATTGGAGGGGTGATCGGGGGCGGTGGGGCTGGAACCTCACCA
51271 ACCGGCGCTGCAGGCACTCGCCCGGGCTCGGGACGTGGTCCCCACTTTAACCTGACCCCTGCGGCGCCTCCGAATGGCGCACCGCAAGGCGT
51363 CGTAAACACCTTAGGTCTGAATGGTGAGCCGTCACGCTCATCCCACCGCGAGCAAGGCGATACTGACGGCCGCTACTGGGATCCCGACCATC
51455 CATGGGCAACCAGCGAGGGCGTTCCTCCAGTAGTCCGCCCGCCCGAGGCGGAGGGACCAATCGACCCAGGGCCAGCTATTGGCTTCGACCGG
51547 TGAAAAACGCTCCTCCAGCGGGCGCTACCTTCACCTTCCTAGCAACATTGATGGTTGCATCAGCGTACGCCCCGAGCGCCGTGCGTGCGA
                                                                                  >  V  R  A
51637 GTCCTGAAACCGATGGTGCCTTGCGAATACGGGCTGACCAGTGGCACCTTAACTACCTGAAGGCGGCGGAGGCTCAGAAGCTGTCACTGGGA
     >S  P  E  T  D  G  A  L  R  I  R  A  D  Q  W  H  L  N  Y  L  K  A  A  E  A  Q  K  L  S  L  G
51729 GAAGGGGTTGTAGTAGCGGTCCCGGATACTGGCGTTGATCCACACCCCGACCTTCAGCGCAATCTAATCAAAGGGATTGACATCATTCCCGG
     >  E  G  V  V  V  A  V  P  D  T  G  V  D  P  H  P  D  L  Q  R  N  L  I  K  G  I  D  I  I  P  G
51821 GGGCAATGGAGATGGCCAGAAAGATCGCAACAGTCACGGCACTAGCATGGCTGGACTAATCGCAGCCCACGGACAGGGCCAGAGCGGCGCCT
     >  G  N  G  D  G  Q  K  D  R  N  S  H  G  T  S  M  A  G  L  I  A  A  H  G  Q  G  Q  S  G  A
51913 TAGGCATAGCACCCAGAGCCAAGATCATGCCAATCCTGTCTTCCGCGTCGAACAACCTCGGTGATGCAGACGGCTTGGCTGCGGGTATAGAA
     >L  G  I  A  P  R  A  K  I  M  P  I  L  S  S  A  S  N  N  L  G  D  A  D  G  L  A  A  G  I  E
52005 TTTGCAATCTCGCATGGGGCGGATGTCATCAATGTCTCCAGCGGAGGCGGCGCCAGCGTTCGACTCATCAAGGCAATCAGAGAGGCGGTCGC
     >  F  A  I  S  H  G  A  D  V  I  N  V  S  S  G  G  G  A  S  V  R  L  I  K  A  I  R  E  A  V  A
52097 CGCAGACATTGTAGTTGTCGCAGCCGCCGGAAACAGTCCCGAAGACATGACAATTGGCTATCCAGCCAGCGAGGAAGGAGTCGTCGCAGTTG
     >  A  D  I  V  V  V  A  A  A  G  N  S  P  E  D  M  T  I  G  Y  P  A  S  E  E  G  V  V  A  V
52189 GCGGAATTGATCGACAGGGAGAGCATGCTTCAGTTTCTGTCGTCGGACCGGAAGTTGACTTAGTCGCACCGGCAGTCGACATCTACAGCACC
     >G  G  I  D  R  Q  G  E  H  A  S  V  S  V  V  G  P  E  V  D  L  V  A  P  A  V  D  I  Y  S  T

52281 AGTTACGACGGGAAGTACTCCAAAGGCACCGGTACGTCCAGTGCCACAGCGATAGTCGCAGGGGCCGCTGCTCTGGTCCGATCGAAGTTTCC
     >  S  Y  D  G  K  Y  S  K  G  T  G  T  S  S  A  T  A  I  V  A  G  A  A  A  L  V  R  S  K  F  P
52373 CGACCTGCCCGCCTCGGAGGTCGTCCATCGCCTCACTGCCACCGCCATCGACAAAGGGCCGCCAGGGCACGACGACCAGTACGGCTACGGCG
     >  D  L  P  A  S  E  V  V  H  R  L  T  A  T  A  I  D  K  G  P  P  G  H  D  D  Q  Y  G  Y  G
52465 TTATCGACCTGGTTGCCGCGCTTACGGCAGACGTACCCCCGGTGGGCTTTGAGTCGGCGACGGCGGACGTGCCCGACGTGCCTGGGTCGACC
     >V  I  D  L  V  A  A  L  T  A  D  V  P  P  V  G  F  E  S  A  T  A  D  V  P  D  V  P  G  S  T
52557 ACGACGGCGGTCGCCGAGCCGGCAGGCGAGGGTGACGATGGGGCAACGGCCCGAGGTCTGGCCACGTTGGGAGTGATCGTGGCTGCTGCGGG
     >  T  T  A  V  A  E  P  A  G  E  G  D  D  G  A  T  A  R  G  L  A  T  L  G  V  I  V  A  A  A  G
52649 CGCTTGGGCGCTGGTCGCTCGACGGCGTAGGTTGAGCGACGACCCGCCCCCGCGGATCAGCCGGTGACCAGCCAGCCCTGACGCCATGTCG
     >  A  W  A  L  V  A  R  R  R  R  L  S  D  D  P  P  P  R  I  S  R  •
52740 GCGACATTGGGGGGTCGGGGTGGGTGGGATACCGCTATTTGGCCGACATGAAGTCGATCAACAGCGATCAACAGGCAGTGTGATCGGCGGGG
```

Figure 11N

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52832 GTCGGTCGACGGCCAGGCGGCGTCGACGGAGGCGGGGGAAGCGGTAGCGTCGGCGACGTGCCGAACTCGATTTCACTCCGACTCGTGCTCGC
                                                                    >V P N S I S L R L V L A
52924 GTCGGCGAGCCCTGCCCGTCGCAAGCTCCTCCACGCCGCCGGCATCGAACCCGACGTGCTGGTCAGTGGGGTCGACGAGTCCCAGGTGACCA
     > S A S P A R R K L L H A A G I E P D V L V S G V D E S Q V T
53016 GCGAGCGAGCCGAGGATCTGTGCCTGGAGCTGGCCCGCCTGAAGGCGCAGGCGGTCGTCGGCCGGCTGCGCCCGTCGGCCGACGAGCGGACG
     >S E R A E D L C L E L A R L K A Q A V V G R L R P S A D E R T
53108 CTGGTGCTCGGCTGCGACTCGGTGCTCGCCTTCGACCGCGAGATTCTCGGCAAGCCGGCCGACGAGGCGGACGCTACCCGGCGTTGGGAGCG
     > L V L G C D S V L A F D R E I L G K P A D E A D A T R R W E R
53200 GATGCGGGGGCGCAGCGGGGTGCTACACACCGGGCACTGCCTGATCGACGTCATCCACGAGACGCGCGCCGAGGCGGTCGCCTCGACCACCG
     > M R G R S G V L H T G H C L I D V I H E T R A E A V A S T T
53292 TGCGTTTCGCTGACATCAGCGACGAGGAGATTGCCGCGTACGTCGCGACGGGCGAACCGCTCGCGGTCGCCGGCGCGTTCACCATCGACGGA
     >V R F A D I S D E E I A A Y V A T G E P L A V A G A F T I D G
53384 ATGGGCGGGGCGTTCCTGGAGGGTGTCGACGGCGACCCGGGCACGGTGGTCGGCCTCTCCCTACCGTTGCTGCGCCGGCTTCTCGGCGAGCT
     > M G G A F L E G V D G D P G T V V G L S L P L L R R L L G E L
53476 GGACCTGCGGATCATCGACCTGTGGACGAAGGTCGCGCCGGGCGGCCAGGCGGTCGAGGCGGTGGGTACGGTCCAGCCATGACGACGAAGT
                                                                    > M T T K
     > D L R I I D L W T K V A P G G Q A V E A V G T V Q P •
53567 CCCTGCCGCTGACCCCGGAACTGCATGCGTACGTGGTGGCCCACGGATCGGACCCGGACGAGGTGATGCGGGATCTGATCGAGGAGACCCTC
     >S L P L T P E L H A Y V V A H G S D P D E V M R D L I E E T L
53659 GCCGCGCTGCCCGCCGAGGCGAGGATGCAGGTGGCCCCGGAGCAAGCCGCGTTCCTGACGTTCCTCACCCGGTTGATCGGGGCGCGGCGGGC
     > A A L P A E A R M Q V A P E Q A A F L T F L T R L I G A R R A
53751 GGTGGAGGTGGGCACCTTCACCGGCCTGTCCTCCCTGGCGATCGCGCGCGGGCTGGCCGAGGGCGGGCGGTTGACCTGCTTCGACATCTCGG
     > V E V G T F T G L S S L A I A R G L A E G G R L T C F D I S
53843 AGGAGTACACGGGCGTCGCGCGGCGGTACTGGGCGCGGGCCGGGGTGGCCGACCAGATCGACCTGCGGATCGGGCCGGCCGGGGACACGCTG
     >E E Y T G V A R R Y W A R A G V A D Q I D L R I G P A G D T L
53935 CGCGGGTTGCCGTACGAACGGCACCTGGACTTCGCGTTCATCGACGCGGACAAGGTCGGCTACCCGGTCTACTGGGCGGAGTTGGTGCCCCG
     > R G L P Y E R H L D F A F I D A D K V G Y P V Y W A E L V P R
54027 CATGCTCCCGGGCGGGGTCATCGCGGTGGACAACACGTTGCGCGGGGGCCGGGTGCTCGCCCCGCGTGACGCCGACGACCGGGCCATCGCCG
     > M L P G G V I A V D N T L R G G R V L A P R D A D D R A I A
54119 CGTTCAACGACGAGGTGATGGCCGACGTCCGGGTGGAGCCGGTGCTGCTGCCGATCGCCGACGGGCTGACCCTGGCCCGGGTGCGCTGACG
     >A F N D E V M A D V R V E P V L L P I A D G L T L A R V R •
54210 GGCGCCAGCCGGACGATCGTGCCAGGTCGCCGGCCCGGCGTCGTGTGTCCGCCTCACCGGGTCGACGAGGGGGTGAGGCGGGGCGGGGTGTT
54302 AGGAAGGGGCCCTTCCTATACCGAATGCGTTAACAAGGGGCCCCTCCTTACACCTCAACCTCAGCGCACGCTGCGGGCGAACTGGCGGGCG
                                                                    < • R V S R A F Q R A
54393 GCCCAGGCGACGCCGACGGCGGCAAGCACCGCGATGATGGTCAGGCCCTGCCAGACCTTGTCGTTGCCGAGGTCGCCGGCGAAGAGGGCCCG
     <A W A V G V A A L V A I I T L G Q W V K D N G L D G A F L A R
54485 GGTGCCGTCCACGGCCCAGGAGAACGGGTTCCACTCGGCGATGCGCTGGAGCCAGCCGGGGGCGAAGGTGAGCGGCAGCAGGATGCCGGAGA
     < T G D V A W S F P N W E A I R Q L W G P A F T L P L L I G S L
54577 GCAGCAGCACCGGCTGGGCGACGGTGTTCATCACCGGGGCGAGCGCGTCCTCACTCTTGAGCGTGACGCCGTACGAGACGGCCGAG
     < L L V P Q A V T N M V P A L A D E S K V K L A V G Y S V A S
54669 GTCATCAGCGCGATCAGGGCGAGCATCAGGTACGCCAGCAGCAGGTCGCCGATGAACACGCGCAGCTCGAACAGGAGCGCGAGCAGGGTGAT
     <T M L A I L A L M L Y A L L L D G I F V R L E F L L A L L T I
54761 GATGACGGCCTGGGCGAGCAGCGACACGACGTCGCGCAGGGCCCGGCCGAGCAGCAGCGCGAGCCGGCTGACCGGGGTGACCCGGGACCGTT
     < I V A Q A L L S V V D R L A R G L L L A L R S V P T V R S R E
54853 CGATGACGCCGGCGCGCAGCTCGGCGATCAGGCCGAAGCCCTGGAAGAGGCCGCCGAAGATGGCCAGCAGCACCAGCAGGCCGGGCACGAAG
     < I V G A R L E A I L G F G Q F L G G F I A L L V L L G P V F
54945 ATCTTGTACGCCTCGGCCTGGGTCGGCGCGTTCAGCGCGGGCTTGAGCAGCGGGGCGAAGAGGAGCAGGTACATCACCGGCTGGAAGACGCC
     <I K Y A E A Q T P A N L A P K L L P A F L L L Y M V P Q F V G
55037 GACGAAGACCCAGACCGGATTGCGGAGCAGGAGTTGCATCTGGCGCTGGGCGACGAGCCAGGTGTCGCGGGCGAACTTCATGATCGGACT
     < V F V W V P N R L L L Q M Q R Q A V L W T D R A F K M
55127 CCGGGTGGTCAGGACTCGCGCAGCGAGCGGCCGGTCTTGGTGAGGAAGACGTCGTCGAGGCTGGGGCGGTGCAGCTCGATCGAGCTGAGCC
           < • S E R L S R G T K T L F V D D L S P R H L E I S S L R
55218 TGAGGCCGGACTGGTCGAGCCGGCGCAGGACCTGCGGGATGGCGGTGGCCCCCTCGTCGACGGTCAGGCGCAGGCCGCCGCCGTCGACGGTT
     < L G S Q D L R R L V Q P I A T A G E D V T L R L G G G D V T
55310 TCCAGCTTGGTGACGTACGGCTCGGTGTCGAGCAGTTGGGCGGCCTGCGGGGTGGCGGCGGTCCAGCCCGACGAGCAGCACCTCGCCGGA
     <E L K T V Y P E T D L L Q A A Q P T A A A D L G V L L V E G S
55402 GATCTCCCGCTTCAGCCCGCCCGGCGTACCCTCGGCGACCACCTCGCCGTGGTCCATGATCGCGATCCGGTCGCAGAGCGCGTCGGCCTCGT
     < I E R K L G G P T G E A V V E G H D M I A I R D C L A D A E D
55494 CCAGGTAGTGCGTGGTGATGAAGACGGTCATCCCCTCGGCGCGCAGCCGACGGATCTCGTCCCACATGTGGGCGCGACTCTGCGGGTCGAGG
     < L Y H T T I F V T M G E A R L R R I E D W M H A R S Q P D L
55586 CCGCTGGTCGGCTCGTCCAGGAAGACAATGCGGGGGTCGTGGATGATGCCGAGAGCGATCTCGACGCGGCGGCGCTGGCCGCCGGAGTAGGT
     <G S T P E D L F V I R P D H I I G L A I E V R R R Q G G S Y T
55678 CTTGCACTTACGGTCGGCGTACTCGGTGAGCTGGAAGGCGGCCAGTGCGCGCTCGGCGCGGCGGAGGGCGTCGGCCTTGCCGATGCCGTACA
     < K C K R D A Y E T L Q F A A L A R E A R R L A D A K G I G Y M
55770 TCCGGGCGTGCAGGACCAGTTCCTCGCGGGCGGTGGAGTCGTCCCAGGTGCTGCCGCCCTGGGCGACATAGCCGATCCGGCGACGCACCTCG
     < R A H L V L E E R A T S D D W T S G G Q A V Y G I R R R V E
55862 GCCGGGTTCCGCAGCAGGTCGGCCCCGGCGATGGTGGCCTGGCCGCCGTCGGGGGTGATGAGGGTGGCCAGCATCCGCAGGGTGGTGGTCTT
     <A P N R L L D A G A I T A Q G G D P T I L T A L M R L T T T K
55954 CCCGGCGCCGTTGGGGCCGAGGAACCCGAAGATCTCCCCCTCGGCGACGTCCAGGTCGACGCCGCGCACGGCGTCGACCGTCTTGTGCTGTC
     < G A G N P G L F G F I E G E A V D L D V G R V A D V T K H Q R
56046 GACCGGCGCGGGAGCGAAACGACTTCCGCAGCCCTCTGGTCTGGATCATCTTCGCTCCTGGTCGTCCTTAGCCGGACCGGGCCGGCCCTC
     < G A R S R F S K R L G R T Q I M
56136 TCTCCGGGACGCCACGCCACACGGGTGGCCCCGAACGTCGCGCCGAGGCTAACGCGATATAACTTCTCTAGTCAACTTTGATTAATGGCGA
                                                                    < • R S I V E R T L K S • H R
56227 CCGTCGGCCCCCTCCCCCACGTTCCAGCCGTCCTGACTGGCCAACCCTTCGGGCAGATACGGCACGCCGGCCTCGATCCGGTCGGCGACCCG
     <G D A G E G V N W G D Q S A L G E P L Y P V G A E I R D A V R
56319 CTCACACCAGGCCACCTCGACCTCTCCCCGGGCAATCCACAGCTCGTACATCCAGCTCACGCCGACCGGCTTGGAGTCGCGGATCCAGGAGG
     < E C W A V E V E G R A I W L E Y M W S V G V P K S D R I W S S
```

Figure 110

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56411 ACTCCATCGAGGCACGCATGGTTTCGACACTGGCCCGCAGCACCTGCCCCCGACTGCGCAGCGCGGCCACCGCCTCCGGCCTGGGCAGCGCC
      <  E  M  S  A  R  M  T  E  V  S  A  R  L  V  Q  G  R  S  R  L  A  A  V  A  E  P  R  P  L  A
56503 GGCAGGAACGCGAACGCCGCCACGAACGGATCGCTCGTCTGATGATTGCCCCACCACAGGCCGCGCAGCAGCGTCTCGAACTCGTCGACCCC
      <P  L  F  A  F  A  A  V  F  P  D  S  T  Q  H  N  G  W  W  L  G  R  L  L  T  E  F  E  D  V  G
56595 CTTCGGGGTGATCTCGTACGTCGTCCGCGCCCGCCGGGCGCCGACCTGCTCGGTGGCGACCTCGCGGAGCAGCCCCTCCTCGCCGAGCTTGC
      <  K  P  T  I  E  Y  T  T  R  A  R  R  A  G  V  Q  E  T  A  V  E  R  L  L  G  E  E  G  L  K  R
56687 GCAGCGCGTGGTAGATCGAGCCGGGCTGCACGTTGGCCCACTTGTCGGCACCCCAACTGAGCAGCTCGCGGCGGACGTCGTAGCCGTGCACC
      <  L  A  H  Y  I  S  G  P  Q  V  N  A  W  K  D  A  G  W  S  L  L  E  R  R  V  D  Y  G  H  V
56779 GGCTGCATCCACTTGACCAGGCCGAGAATCATCATGCGAGTGGCAGACACCGGAAAAGCGTATTAGACAAGTTTGACTATCCAAGCATCTG
      <P  Q  M  W  K  V  L  G  L  I  M  M
56870 GGCAGTGCCTCATCCCACACTGAGCGATCGTTAGGGCCACGACGCCGGCCGATAAACTCCCCGTCAGTAACATCCCGGGAGGAGCCACGAG
56961 GTGCGCAAGGTACTCATCGCCAACCGAGGCGAGATCGCCGTCCGCGTCATCCGCGCCTGCCGCGACGCCGGCCTGGGCAGCGTCGCCGTCT
      >  V  R  K  V  L  I  A  N  R  G  E  I  A  V  R  V  I  R  A  C  R  D  A  G  L  G  S  V  A  V
57052 ACGCGGACTCCGACCGGGACGCCCTGCACGCGACCCTGGCCGACGAGGCGTACGCCCTGGGCGGCGACACCGCCGCCGAGACGTACCTGCGG
      >Y  A  D  S  D  R  D  A  L  H  A  T  L  A  D  E  A  Y  A  L  G  G  D  T  A  A  E  T  Y  L  R
57144 ATCGACAAGCTGATCGCCGTCGCGGCACAGGCCGGGGCCGACGCCGTCCACCCCGGGTACGGCTTCCTCGCCGAGAACGCCGACTTCGCCCA
      >  I  D  K  L  I  A  V  A  A  Q  A  G  A  D  A  V  H  P  G  Y  G  F  L  A  E  N  A  D  F  A  Q
57236 GGCCGTCCTCGACGCCGGGCTTACCTGGATCGGCCCGACCCCACAGGCGATCCGCGACCTGGGCGACAAGGTCACCGCCCGGCACATCGCCC
      >  A  V  L  D  A  G  L  T  W  I  G  P  T  P  Q  A  I  R  D  L  G  D  K  V  T  A  R  H  I  A
57328 AGCGGGCCGGCGCGCCCCTGGTTCCCGGTACCTCGGACCCGGTCGGCAGCCCGGACGAGGTGATCGCATTCGCGGTCGACCACGGCCTGCCG
      >Q  R  A  G  A  P  L  V  P  G  T  S  D  P  V  G  S  P  D  E  V  I  A  F  A  V  D  H  G  L  P
57420 GTCGCCATCAAGGCCGCCTTCGGCGGCGGCGGGCGCGGCCTCAAGGTGGCCCGCACGATGGAGGAGATCCCGCACCTGTTCGAGTCGGCCAC
      >  V  A  I  K  A  A  F  G  G  G  G  R  G  L  K  V  A  R  T  M  E  E  I  P  H  L  F  E  S  A  T
57512 CCGGGAGGCGGTCGCGGCGTTCGGCCGGGGCGAGTGTTTCGTCGAGCGGTACCTCGACCAGCCCCGGCACGTCGAGGCCCAGGTCCTCGCCG
      >  R  E  A  V  A  A  F  G  R  G  E  C  F  V  E  R  Y  L  D  Q  P  R  H  V  E  A  Q  V  L  A
57604 ACCAGCACGGCAACGTGATCGTCGTCGGCACCCGGGACTGCTCGCTGCAACGCCGGCACCAGAAACTCGTCGAGGAGGCCCCCGCGCCGTTC
      >D  Q  H  G  N  V  I  V  V  G  T  R  D  C  S  L  Q  R  R  H  Q  K  L  V  E  E  A  P  A  P  F
57696 CTCACCGACGCCCAGCGCCGGCAGATCCACGACAGCGCCAAGGCAATCTGCCGGGAGGCCGGCTACCACGGCGCCGGCACCGTGGAGTACCT
      >  L  T  D  A  Q  R  R  Q  I  H  D  S  A  K  A  I  C  R  E  A  G  Y  H  G  A  G  T  V  E  Y  L
57788 GGTGGGCACGGACGGCACGATCTCCTTCCTTGAGGTCAACACCCGCCTGCAGGTCGAGCACCCGGTCACCGAGGAAACCGCCGGCATCGACC
      >  V  G  T  D  G  T  I  S  F  L  E  V  N  T  R  L  Q  V  E  H  P  V  T  E  E  T  A  G  I  D
57880 TCGTCCGCGAGCAGTTCCGGATCGCCGACGGCGAGAAGCTGCGGCTGGCCGAGGATCCGACCCCGCGCGGGCACTCCATCGAGTTCCGGATC
      >L  V  R  E  Q  F  R  I  A  D  G  E  K  L  R  L  A  E  D  P  T  P  R  G  H  S  I  E  F  R  I
57972 AACGGCGAGGATCCGGGCCGCAACTTCCTGCCCGCCCCCGGCACCGTCACCGCGCTGCGGCTGCCCACCGGCCCCGGTGTCCGGGTGGACAC
      >  N  G  E  D  P  G  R  N  F  L  P  A  P  G  T  V  T  A  L  R  L  P  T  G  P  G  V  R  V  D  T
58064 CGGCATCTCCGCCGGCGACGTGATCGGCGGCAACTTCGACTCCCTGCTGGCCAAGGTGATCATCACGGGCGAGACCCGCACCGAGGCCCTGG
      >  G  I  S  A  G  D  V  I  G  G  N  F  D  S  L  L  A  K  V  I  I  T  G  E  T  R  T  E  A  L
58156 AGCGGGCCCGGCGGGCGCTGGACGAGATGGTCGTCGAGGGAATGGCCACGGCGCTGCCGTTCCACCGCCTGGTGGTACGCGACCCCGCGTTC
      >E  R  A  R  R  A  L  D  E  M  V  V  E  G  M  A  T  A  L  P  F  H  R  L  V  V  R  D  P  A  F
58248 ACCGCCGCGCCGTTCACCGTGCACACCCGGTGGATCGAGACGGAGTTCGACAACACCGTCCTGCCGTTCACCGCCGCCGCCGGCCCCGCCGA
      >  T  A  A  P  F  T  V  H  T  R  W  I  E  T  E  F  D  N  T  V  L  P  F  T  A  A  A  G  P  A  E
58340 GGGCCCGGCCGAGCGGGAGACCGTCGTGGTCGAGGTGGGCGGCAAGCGGCTGGAGGTGACCCTCCCCGCCGGCCTCGGCGCGGGTACGGCCG
      >  G  P  A  E  R  E  T  V  V  V  E  V  G  G  K  R  L  E  V  T  L  P  A  G  L  G  A  G  T  A
58432 CCGGGCCCGCCGCGCGGAAGCCGGCCCGGGGCGGCGGGCCAAGGCCGGCGCGGCTGGCGGCGACGCCCTCACCTCTCCGATGCAG
      >A  G  P  A  A  R  K  P  A  R  R  G  G  G  A  K  A  G  A  A  V  G  G  D  A  L  T  S  P  M  Q
58524 GGCACGATCGTGAAGATCGCCGTCGCGGACGGGGACACCGTCGCCAAGGGCGACCTGGTCGTCGTGCTGGAGGCGATGAAGATGGAGCAGCC
      >  G  T  I  V  K  I  A  V  A  D  G  D  T  V  A  K  G  D  L  V  V  V  L  E  A  M  K  M  E  Q  P
58616 GCTGCACGCGCACAAGGCGGGCACGGTCGGCGGGCTGTCCGCCGAGGTCGGCGCGGTCCTCGCCGCCGGCGCCCCCATCTGCACCATCACCT
      >  L  H  A  H  K  A  G  T  V  G  G  L  S  A  E  V  G  A  V  L  A  A  G  A  P  I  C  T  I  T
58708 GAGGTGCAAGGAGGGGCCCCCTGTTAACGCATTCGGTATAGGAAGGGCCCCTTCCTAACCACGCGCCCGGCGGGGCCGCGCCCCAGCCCGGG
      >•
58800 TACGCGTACCGGCCGGGGGTGTTTTCCGCGACCACCGCGAGCGGTGAGGACCGGGGCCGGGAATGATGGCCAGGTGCGGTTCCTACATGGC
                                                                  >  >  V  R  F  L  H  G
58891 GCGGTTCCCGCGCACGACCTGACCTACAACGACGTCTTCATGGCGCCGAACCGCTCCGAGGTCGGCTCCCGGTTGGACGTCGACCTGGCCAC
      >  A  V  P  A  H  D  L  T  Y  N  D  V  F  M  A  P  N  R  S  E  V  G  S  R  L  D  V  D  L  A  T
58983 CTCCGACGGCACGGGCACCACCATCCCGCTGGTGGTGGCGAACATGACGGCGGTGGCCGGCCGGCGGATGGCCGAGACTGTCGCCCGGCGGG
      >  S  D  G  T  G  T  T  I  P  L  V  V  A  N  M  T  A  V  A  G  R  R  M  A  E  T  V  A  R  R
59075 GCGCACTCGCGGTGATCCCGCAGGACATCCCGATCGAGGTGGTGGCCAACGTGGTCGCCTGGGTCAAGCAACGGCACCTGGTGCACGACACG
      >G  A  L  A  V  I  P  Q  D  I  P  I  E  V  V  A  N  V  V  A  W  V  K  Q  R  H  L  V  H  D  T
59167 GCGATCACGCTCGGCCCCACCGACACCGTCGGCGATGCCATCCATCTGCTGCCGAAACGGTCGCATGGCGCGGTGGTGGTGGTCGACGAGGC
      >  A  I  T  L  G  P  T  D  T  V  G  D  A  I  H  L  L  P  K  R  S  H  G  A  V  V  V  V  D  E  A
59259 CGGTCGGCCGCTGGGCGTGGTGACGGAGGCGGACACCGTCGGGGTGGACCGCTTCGCCCAGCTCCGCCACGTGATGTCGACCGAGTTGCACA
      >  G  R  P  L  G  V  V  T  E  A  D  T  V  G  V  D  R  F  A  Q  L  R  H  V  M  S  T  E  L  H
59351 CGGTGCCGGCGGACGCGGACCCGCGTACCGGATTCGACCGGCTCTCGGCGGGCCGGCGGCGGCTCGCGCCGGTGGTGGACGGCGACGGCCGG
      >T  V  P  A  D  A  D  P  R  T  G  F  D  R  L  S  A  G  R  R  R  L  A  P  V  V  D  G  D  G  R
59443 CTCGTCGGGGTGTTGACCCGCAAGGGCGCGCTGCGCGCGACCCTCTACACCCCGGCGGTGGACGACCGGGGCCGGCTGCGGATCGCGGCGGC
      >  L  V  G  V  L  T  R  K  G  A  L  R  A  T  L  Y  T  P  A  V  D  D  R  G  R  L  R  I  A  A  A
59535 CGTCGGCATCAACGGCGACGTCACCGGCAAGGCCGCCGCGCTGCTGGAGGCCGGGGTCGACGCCCTGGTGGTGGACACCGCGCACGGCCACC
      >  V  G  I  N  G  D  V  T  G  K  A  A  A  L  L  E  A  G  V  D  A  L  V  V  D  T  A  H  G  H
59627 AGGCGCGGATGGTCGCCGCGCTGCGGGCGGTGCGCAAGCTTCACCCGGGCGTTCCGGTCGCGGCCGGCAACGTGGTCACCGCCGATGGGGTA
      >Q  A  R  M  V  A  A  L  R  A  V  R  K  L  H  P  G  V  P  V  A  A  G  N  V  V  T  A  D  G  V
59719 CGCGACCTCGTCGAGGCCGGCGCCGACATCGTGAAGGTGGGCGTCGGTCCGGGCGCGATGTGCACCACCCGGATGATGACCGGGGTGGGGCG
      >  R  D  L  V  E  A  G  A  D  I  V  K  V  G  V  G  P  G  A  M  C  T  T  R  M  M  T  G  V  G  R
59811 TCCGCAGTTCTCCGCGGTGCTGGACTGCGCGGCGGCGGCGCGGGACCTCGGCCGGCACGTCTGGGCCGACGGCGGGGTACGGCACCCGCGCG
      >  P  Q  F  S  A  V  L  D  C  A  A  A  A  R  D  L  G  R  H  V  W  A  D  G  G  V  R  H  P  R
59903 ACGTGGCGCTGGCCCTCGCCGCCGGCGCGTCGAACGTGATGATCGGTTCCTGGTTCGCCGGCACGTACGAGTCCCCGGGTGACCTGTACACG
      >D  V  A  L  A  L  A  A  G  A  S  N  V  M  I  G  S  W  F  A  G  T  Y  E  S  P  G  D  L  Y  T
59995 GACGCGGACGGCCGGAGGTACAAGGAGAGCTTCGGGATGGCCTCGTCGCGGGCGGTCAGCGCGCGTACGGCCGAGGACAGCGCGTTCGACCG
      >  D  A  D  G  R  R  Y  K  E  S  F  G  M  A  S  S  R  A  V  S  A  R  T  A  E  D  S  A  F  D  R
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Figure 11P

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60087 GGCCCGCAAGGGGATCTTCGAGGAGGGCATCTCCTCGGCCCGGATGTACCTCGACCCGGATCGCCCGGGCGTCGAGGACCTGATCGACGAGA
      > A R K G I F E E G I S S A R M Y L D P D R P G V E D L I D E
60179 TCATCTCCGGGGTACGCAGCGCGTGCACGTACGCGGGCGCGCGCAGCCTGGCGGAGTTCGCGGAGCGGGCGCTGGTCGGGGTGCAGAGCACG
      >I I S G V R S A C T Y A G A R S L A E F A E R A L V G V Q S T
60271 GCCGGCTACACCGAGGGGATGCCCCTACCGACGAGTTGGTGACCCCGCGCCCGGCGGTGAGAAGGGTTCCCCTCTCTACCGGAGGCGTCAA
      > A G Y T E G M P L P T S W •
60362 CAAGGGGCCCTTCCTTCGTGCGCGGCTGGGTATCGGCGTGACCGACTGCCGCACGCGCCGCCGCCACACTGAGCCGCCGCCCGTCGAGGGCCC
60454 ACCGAACGGGCGCCGGGGTCAGTCGAAGAGGCGACGGATGACGGTCCGGGCGGCGGCCTCCGGGTCCGGGCCGGTGCCGGGCGGGAGCGCC
                        < • D F L R R I V T R A A A E P D P G T G P P L A
60545 CCGGCCAGCCAGAGTGTCACGAAGCCGTGCACGATCGACCAGGCGGCCAGGGCGTCCGCCTCCTGGTCCGGGTCGGTTTCCCGGCGCGGGAG
      <G A L W L T V F G H V I S W A A L A D A E Q D P D T E R R P L
60637 GGCGGCCACCCCGGCCCGCAGCGCCGCGCCGGCCCGATCACGGGCGGCTGTCACCTCGGGGTCGTCGCGACGGTAGAGCTCCGGGCGGAACA
      < A A V G A R L A A G A R D R A A T V E P D D R R Y L E P R F M
60729 TCACCTCGAAGTGGGCCCGGTGGTCGACCGCGAACCGGACGTACGCCACGCCGGCGTCGAGCAGGTCGCCGGCCTCGCACAGCGCCCCGGCC
      < V E F H A R H D V A F R V Y A V G A D L L D G A E C L A G A
60821 AGCAGGTCGAATCCCTCGACGGCGAGCGCGGTGAGCAGCCCCGCCTTGTCGCCGAAGTGGTGCGCGGGGGCGGCGTGCGAGACCCCGGCCCG
      <L L D F G E V A L A T L L G A K D G F H H A P A A H S V G A R
60913 GCGGGCCAGGTCGCGCAGGCTCAGGGCGGCCGGCCCGGCGTCGGTGATCGCGTCGACGGCGGCGGCGAGCAGGGCGCGACGCAGGTCACCGT
      < R A L D R L S L A A P G A D T I A D V A A A L L A R R L D G H
61005 GATGGTAGCCACGCGGTCCGGTCATGCCGGCAGCCTAACTTGTCATTGACAAGATAGCCAGGCCGAAGCAATCTAGGCAATGACAAGTTG
      < H Y G R P G T M
61095 CCTTCGACCGAGGAGAACCCCGATGGCGCCCCTGATCGCTCTCATCGCCGGCTCGGCCCTGGCCCGACTCGCCGGGCTACTCAACGTCGACG
61187 CCCTGGCCGGCTGGCACCCCGCCCTGCGGGTCGGGCTCGCGGCCATGTTCGCGCTCACCGGGATCGCCCACTTCACCTCCCGACGGCCCGAC
61279 CTGGTCGCCATGGTGCCGCCCCGACTGCCCCACCCGGGGCTGCTGGTGACCGTCACCGGCCTGCTGGAGTTGGCCGGCGCGGTCGCGCTGCT
            > M V P P R L P H P G L L V T V T G L L E L A G A V A L L
61371 CGTCCCCGGCACGGCGCGGTGGGCAGCGGCCGGGCTGGGGCTGCTGCTGCTCGCGATGTTCCCGGCCAACGCCTCGGCCGCCCGGCGCGGGC
      > V P G T A R W A A A G L G L L L L A M F P A N A S A A R R G
61463 TGACCCTGGCCGGCCGGCCGGTGACCCCGCTCGTCCCCCGCGCGCTGCTCCAGGTGATCTTCCTCACCGCCGCCGCCGCGATTTCGTTTGGG
      >L T L A G R P V T P L V P R A L L Q V I F L T A A A A I S F G
61555 CCCTGACTATCAGGGAGCTAACATGACCCGCATGGAGCTGATAGGGCTGCGAGACGTGCCACTCGGCCGGCTGCTGGTGACCGCCGGCCA
      > P •                                                    > V P L G R L L V T A G H
61645 CGTCGTCGGCCAACGGTGGAACCGCTACCTCGCCGAGGAGCACGGCCTCACCCAGGCGGGCATGGTCACCCTGATGACCCTGGCCCGGCACG
      > V V G Q R W N R Y L A E E H G L T Q A G M V T L M T L A R H
61737 GCGAGCTGCCGCACCGGGCGGTCGCCGAGGCGTGCTTCATCCGCCCGGCCACCCTAACCGGCATCGTCGACACACTGGAGCGCGACGGCCTC
      >G E L P H R A V A E A C F I R P A T L T G I V D T L E R D G L
61829 GTCGAGCGGCAACGCGACGACGTCGACCGGCGCAGCGTGCGGCTCGTCCTGACCCCCGCCGGTCGGGAACGGGTCGCCGCGCTCACCAACGT
      > V E R Q R D D V D R R S V R L V L T P A G R E R V A A L T N V
61921 CATGCAGTCCGGACGACCGATGACCTCGGTCGACGCCGACCCGGCGAAGGCCGCCGTGATCCGGCAGTTCCTGCTCGAGGTCATCGGCAGTG
      > M Q S G R P M T S V D A D P A K A A V I R Q F L L E V I G S
62013 GAGAGGAACCTCGGGTGACGGCCCTCGACGCGAGGCCGGAGGCTCCGGCATGCTGATCCGGCTGCTCCGCGCCCACCTGCGCCCGTACCGTC
      >G E E P R V T A L D A R P E A P A C •
62105 GACCGCTGGCGGCGGTGATGGCGTTGCAGTTCGTCGGCACGATGGCCTCGCTCTACCTGCCGAGCCTCAACGCCGACATCATCGACCAGGG
                        > M A L Q F V G T M A S L Y L P S L N A D I I D Q G
62196 TGTGGCCCGGGGCGACACCGGCTACATCATGCGTACGGGCGGCTGGATGCTGCTGGTCAGCCTGGTGCAGATCGCCTGCTCCACCGCCGCGG
      > V A R G D T G Y I M R T G G W M L L V S L V Q I A C S T A A
62288 TCTTCCTCGGCGCGCGCTCCGCGATGGGCTTCGGCCGGGACGTACGCGCCGAGGTCTTCGCCCACGTCAACCGGTTCTCCGCCCGCGAGGTG
      >V F L G A R S A M G F G R D V R A E V F A H V N R F S A R E V
62380 ACCCGCTTCGGCGCACCCTCGCTGATCACCCGCAACACCAACGACGTGCAACAGGTGCAGATGCTCGTCCTGATGAGCTGCACCATGCTGGT
      > T R F G A P S L I T R N T N D V Q Q V Q M L V L M S C T M L V
62472 CGCCGCGCCGATCATGAGCGTCGGCGGGGTGTTCATGGCACTGCGGGAGGACGTCGGGCTGTCCTGGCTGATGCTGGTCAGCGTGCCGGCGC
      > A A P I M S V G G V F M A L R E D V G L S W L M L V S V P A
62564 TGGCGATCGCCCTGATGCTGATCATCCGGCGGATGGTGCCCGGGTTCCGGCTGATGCAGACCCGCATCGACGCGGTCAACCGCGTGCTGCGC
      >L A I A L M L I I R R M V P G F R L M Q T R I D A V N R V L R
62656 GAGCAGATCACCGGCATCCGGGTGGTCCGGGCGTTCGTCCGCGAGCCGTACGAGACGGCGCGCTTCGGCCGCGCGAACGCCGACCTCACCGC
      > E Q I T G I R V V R A F V R E P Y E T A R F G R A N A D L T A
62748 GACCGCCCTGCGCACCGGTCGGTTGATGGCCCTGATCTTCCCCGTGGTGACGCTGGTGCTCAACGTCTCCAGCGTCGCCGTGCTGTGGTTCG
      > T A L R T G R L M A L I F P V V T L V L N V S S V A V L W F
62840 GCGCGGACCGCGTCGACGCCGGCCAGATCCAGGTCGGCGCGCTCACCGCCTTCCTGCAGTACCTCATGCAGATCCTGATGGCCGTCATGTTG
      >G A D R V D A G Q I Q V G A L T A F L Q Y L M Q I L M A V M L
62932 GCCACCTTCATCCTGATGATGGTCCCGCGCGCCGCGGTCTGCGCCGAGCGGATCGTCGAGGTGCTCGACACCGACTCGACGGTGATCCCGCC
      > A T F I L M M V P R A A V C A E R I V E V L D T D S T V I P P
63024 GGCCGCGCCGACGGCCGAGGTGACCGGCCGGGGCGAACTGGAACTGCGCGGCGTCCGGTTCCAGTACCCGGGGGCGAGCGCGCCGGTGCTGC
      > A A P T A E V T G R G E L E L R G V R F Q Y P G A S A P V L
63116 ACGACATCTCGTTCCGGGCCACGCCCGGGCGCACCACGGCCATCATCGGCAGCACGGGGGCCGGCAAGACGACCCTGCTGACGCTGATCCCC
      >H D I S F R A T P G R T T A I I G S T G A G K T T L L T L I P
63208 CGGCTGATCGACGCCACCGCCGGGGCGGTGCTGGTCGACGGGGTGGACGTGCGTGACCTGGCCCCGGACGATTTGTGGCGGCGGATCGGGCT
      > R L I D A T A G A V L V D G V D V R D L A P D D L W R R I G L
63300 GGTGCCGCAGCGGCCGTACCTGTTCAGCGGCACGATCGCCAGCAACCTGCGGTACGGCAACCCGGACGCCACCGACGCGGAGCTGTGGGCCG
      > V P Q R P Y L F S G T I A S N L R Y G N P D A T D A E L W A
63392 CCCTGGAGATCGCCCAGGCGCGCGACTTCGTCGCCGAGTTGCCCGAAGGGCTGAACGCCCCGATCACGCAGGGCGGCACCAATATCTCCGGC
      >A L E I A Q A R D F V A E L P E G L N A P I T Q G G T N I S G
63484 GGGCAGCGCCAGCGCCTCGCGATCGCCCGGGCCCTGGTCCGCAAGCCGGAGATCTACCTGTTCGACGACTCGTTCTCGGCGCTCGACCTGGG
      > G Q R Q R L A I A R A L V R K P E I Y L F D D S F S A L D L G
63576 CACCGACGCCCGGCTGCGCGCGGCGCTACGACCGGTCACCGCGGACGCGACGGTGCTGATCGTGGCCCAGCGGGTCTCCACGATCGTCGACG
      > T D A R L R A A L R P V T A D A T V L I V A Q R V S T I V D
63668 CCGACCAGATCATCGTGCTTGAGGACGGGGGCATCGTCGGGATGGGCCGACACGCCGAACTACTGGAAGACTGCCCGACGTACGCGGAGATC
      >A D Q I I V L E D G G I V G M G R H A E L L E D C P T Y A E I
63760 GTCGCCTCCCAGCAGACGGCGGGGGTGCCGGCATGACGGCCGTACCGGATCAGCGGCCCACCGCGCGGCCGGCGGAGGGGCCGACGCCGAA
      > V A S Q Q T A G V P A •
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Figure 11Q

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63851 GCGGCTGCCCTCCGGCAACCAGGGCAGCGGCCCGAGGTGGATGAGCGCCGGCATGCCGGCCGAGAAGTCGATGAACTTCGGGCCGTCCAC
                                                    >M S A G M P A E K S M N F G P S T
63941 CCGCCGGCTGCTGCGCCGGCTGCGACCGCACCGCCTCCAGCTGGCCGCCATCGTCCTGCTCTCGCTGGTCAGCGTCGGTTGCAACGTGTACG
      > R R L L R R L R P H R L Q L A A I V L L S L V S V G C N V Y
64033 GGCCGAAGGTGCTCGGCCACGCCACCGACCTGATCTTCAGCGGGGTGATCGGCCGGCAGTTGCCGGCCGGCACCACCGCCGAGCAGGCGGTC
      >G P K V L G H A T D L I F S G V I G R Q L P A G T T A E Q A V
64125 GCGGCGGCCCGCGCGGCCGGTAACGACAGCTTCGCCGACATGCTGGCCCGGATGGACGTGGTGCCCGGGGTGGGCATCGACTTCACCGCCCT
      > A A A R A A G N D S F A D M L A R M D V V P G V G I D F T A L
64217 GGGCCGGGTGCTGCTGTTCGTGCTCGCCCTCTACCTGGCGGCCAGCGTGCTGTTGTGGTGGCAGGGCTGGCTGCTCAACGGGGTGGTGCAGC
      > G R V L L F V L A L Y L A A S V L L W W Q G W L L N G V V Q
64309 GCACGGTGCTGCGGCTGCGCGCCGACGTGGAGGACAAGCTGAACCGGCTGCCGCTGCCGTACTTCGACCGGCAGCCCCGGGGCGAGTTGCTC
      >R T V L R L R A D V E D K L N R L P L P Y F D R Q P R G E L L
64401 AGCCGGGTCACCAACGACATCGACAACATCTCGCAGAGCCTCCAGCAGACGCTGAGCCAGCTGCTCACCTCGCTGCTCACCGTGGTCGGCGT
      > S R V T N D I D N I S Q S L Q Q T L S Q L L T S L L T V V G V
64493 ACTGGCCATGATGTTCTGGATCTCGCCGCTGTTGGCGCTGGTGTCCCTGGTCGCGGTGCCGATGTCGGTGGTGGTCACCAGCCTGGTCGCGA
      > L A M M F W I S P L L A L V S L V A V P M S V V V T S L V A
64585 AGCGGTCACAGCAGCGGTTCATCGCCCAGTGGACGCATACCGGAGAGCTGAACGGCCAGATCGAGGAGGCGTTCACCGGACACGAGCTGGTC
      >K R S Q Q R F I A Q W T H T G E L N G Q I E E A F T G H E L V
64677 AAGGTCTTCGGCCGGCAGCGCGAGGTGGAGGCCGCCTTCACCGCCAAGAACGAGGAGCTGTTCCGGGCCAGCTTCGGCGCCCAGTTCATCTC
      > K V F G R Q R E V E A A F T A K N E E L F R A S F G A Q F I S
64769 CGGGATCATCATGCCGGCGATGATGTTCATCGGGAACCTCAGCTACGTCGCGATCGCCGTGGTCGGCGGGCTGCGGGTGGCGTCGGGGTCGA
      > G I I M P A M M F I G N L S Y V A I A V V G G L R V A S G S
64861 TGAGCATCGGCGACGTGCAGGCATTCATCCAGTACTCCCTCCAGTTCACCCAGCCGCTGACCCGGGTCGCCTCGATGGCCAACCTGCTCCAG
      >M S I G D V Q A F I Q Y S L Q F T Q P L T R V A S M A N L L Q
64953 TCCGGGGTGGCCTCCGCCGAGCGGGTGTTCGCGGTGCTCGACGCCGAGGAGCAGAGCCCGGACCCGGCGGTGCCGGCCCGGGTCGCCGACCA
      > S G V A S A E R V F A V L D A E E Q S P D P A V P A R V A D Q
65045 GCGCGGTCGCGTCGAATTCGACCACGTCTCATTCCGGTACGAGCCGGACAAGCCGCTGATCACCGACCTGTCGCTGGTCGCCGAGCCGGGGC
      > R G R V E F D H V S F R Y E P D K P L I T D L S L V A E P G
65137 ACACGGTTGCCATCGTCGGGCCGACCGGCGCCGGCAAGACCACCCTGGTCAACCTGGTGATGCGCTTCTACGAGCTGGACGCCGGCCGGATC
      >H T V A I V G P T G A G K T T L V N L V M R F Y E L D A G R I
65229 ACCCTCGACGGGGTCGACATCACCACGCTGAGCCGCGACGACCTGCGCGGCCGGATCGGCATGGTGCTCCAGGACACCTGGCTCTTCGGTGG
      > T L D G V D I T T L S R D D L R G R I G M V L Q D T W L F G G
65321 CACGATCCGCGACAACATCGCGTACGGCCGGCCGGACGCGAGCGAGGAGGAGATCGTCGCCGCCGCCCCGGGCGACGTTCGTGGACCGGTTCG
      > T I R D N I A Y G R P D A S E E E I V A A A R A T F V D R F
65413 TGCGTAGCCTCCCCGACGGCTACGACACCGTCATCGACTCCGAGGGCAGCAACGTCAGCGCCGGCGAGAAGCAGCTCATCACCATCGCCCGG
      >V R S L P D G Y D T V I D S E G S N V S A G E K Q L I T I A R
65505 GCGTTCCTGGCCGAGCCGTCGCTGCTGATCCTCGACGAGGCGACCAGTTCGGTGGACACCCGCACGGAGGTGCTGCTCCAACGGGCCATGGC
      > A F L A E P S L L I L D E A T S S V D T R T E V L L Q R A M A
65597 GGCGCTGCGCTCGGACCGGACCAGCTTCGTCATCGCCCACCGTTTGTCCACCATCCGCGACGCGGACCTGATCCTGATGATGGAGCACGGTC
      > A L R S D R T S F V I A H R L S T I R D A D L I L M M E H G
65689 GCATCGTCGAGCAGGGCACCCACGAGCAGCTCCTGGCCGCCCGGGGCGCGTACCACCGGCTTTACCAGGCCCAGTTCACCCAGCCGGACCCG
      >R I V E Q G T H E Q L L A A R G A Y H R L Y Q A Q F T Q P D P
65781 GCCGCCGTCGGGGACCCCGAGCCCCAGCCCGCCTCGGTCCGGGGCTGACCGTCGTGGCCCGGTACATCCCGCCCAGCTCCCCGACCCGCAG
      > A A V G D P E P Q P A S V R G •
65872 GGGCAGCTCCCGGGGCCCCGGGCGCGGAAGACCAGAGCGTGGTGCGGGCAGAGCGCCGGGCGGAGCACGAACTCGTCGTCGGGGCCCAGCCG
65964 CATCGGCGGGAACATGTCGTCGGCGAAGTGGCCGAGGTCGGGGCCTCGATGACGGTGACGTCAGTGCGGCGCGCCGGGGTTCCCCGACGTCG
66056 TGGTCCGTACCGCGCTGCGCATGGGGAGACGGTAGGCCGGCCGGGGGCGGGCGCGCATCCGAATTCGGGGCCGGCCCGACGCAGCCGAGACG
66148 CATCCGGTTACCGCGAAGGGCGACAGGCCGCCAGTCGCTACAGTCGGCAACCCGGCCGATGCACAGCGCGCCTCGGGGCGGGCCGCCGGCAC
66240 GGGACCTGCCGGCGGCCCATGGCGGCCCGGTCGTCGGCTACGGGGGGTCCGACACTCGAGGCCGCGCCGACTACGGTACGCCGGCCGTCGGC
66332 GATCCGCCGACCGCCTCCACCCGTACGCCGAGGTTGCCGGCCCCAGCGGGTCCCCGGCCCGCCGCGCTGCCCGACCGCCGCGTCGCCGGCCC
66424 GACGACCCGGTTCGTGGCGGGTGCCGGCGAGGTGGAGCCGCCCAGTTACTCCAGCTCGTGGAGCATGAGCTGGCGGGCGGCCTCGGTGATC
                                                    < • E L E H L M L Q R A A E T I
66515 GAGCCCGACAGGCTCGGGTAGATGGTGATGGTCTGGGCCAACTCGTTGACCGTGAGGTTGTTCTCCACCGCCATGGTGATCGGCAGGATCAG
      <S G S L S P Y I T I T Q A L E N V T L N N E V A M T I P L I L
66607 CTCGCTGGCCTTCGGTGCCACCACCACACCGCCGATCACCTGGCCGCTGGCCGGGCGGCAGAACAGCTTCACGAAGCCGTCGGCGAGGTCGT
      < E S A K P A V V V G G I V Q G S A P R C F L K V F G D A L D D
66699 CCATCTTCGCCCGGGCGTTGCCCGACAGCGGCAGCATCACCTGGCGGGCCGGGGTCTTGCCGGCGTCCACCTCGTCCTGGGAGACGCCGACG
      < M K A R A N G S L P L M V Q R A P T K G A D V E D Q S V G V
66791 GTGGCCAACTCCGGGTCGGTGAAGACGTTCGCGGCCACCGTACGCAGCCGCAGCGGCCGGACCGCCTCGCCGAGCGCGTGCCACATCGCGAT
      <T A L E P D T F V N A A V T R L R L P R V A E G L A H W M A I
66883 CCGGCCCTGCATGGCGGCGACGCTGGCCAGCGGCAACACCCCGGTGCAGTCGCCGGCAGCGTAGATCCCGGGGACGTTGGTGCGGGACACCC
      < R G Q M A A V S A L P L V G T C D G A A Y I G P V N T R S V R
66975 GGTCGACGGTGACGTAGCCGCCCCGGGCCAGCTCGACGCCGTACTCGGCGAGGCCGAGGTTGGCGGTGTTGGGGATCGAGCCGACCGCGATG
      < D V T V Y G G R A L E V G Y E A L G L N A T N P I S G V A I
67067 AGCGCGTGCGAGCCGTGCACCAGCCGGCCGTCGGCCAGTTCGACCTCCACCCCGTCGGCGATGCGCTGGACCCTCTCGGCGCGGGAGTTGTT
      <L A H S G H V L R G D A L E V E V G D A I R Q V R E A R S N N
67159 GAGGATCGTCATGCCCCGGGAGCGGAACACGCGCTCGATCGCCATGGCGGCGTCGGCGTCCTCGTGCGGCATCACCCGGTCCCGGCTGGAGA
      < L I T M G R S R F V R E I A M A A D A D E H P M V R D R S S V
67251 CGAGGGTGACCGGGACCCCCATGGCCAGGTACGCGCTGGCGAACTCGGCACCGGTGACGCCGGAACCGACGACGATCAGGTGCTCGGGCAGG
      < L T V P V G M A L Y A S A F E A G T V G S G V V I L H E P L
67343 TGCGGCAGGTCGTACACCTGCCGCCAGGTCAGGATGCGCTCGCCGTCCGGCACGGCCGTGGGGAGCTGGCGGGGGGTGGCGCCGGTGGCGAC
      <H P L D Y V Q R W T L I R E G D P V A T P L Q R P T A G T A V
67435 CAGCACGGTCGACGCGTCGATCGAGTGCTTCTCGGAGCCGTCGGCCGGCGTGACGACGACGCGGTGGGTGTGGCCCAGCATGTCCTCGCCGA
      < L V T S A D I S H K E S G D A P T V V V R H T H G L M D E G L
67527 GCCGGGCCGTGCCGGCCACGAAGGTGACGCCGGCTTTCACCAGCTTCGCGTGGATGTCGGCGGACTGGGCCAGGGCGAGCCGCTTGACCCGC
      < R A T G A V F T V G A K V L K A H I D A S Q A L A L R K V R
67619 TCGTGCACGGCCCGGGCGTCGACGGTGACCGCCTCCAGCCCGTCGGAGTGCACCCCGAACTCCTCGGTGTCCCGGTACCCGGTGACCACCTC
      <E H V A R A D V T V A E L G D S H V G F E E T D R Y G T V V E
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Figure1R

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67711 CGAGCTGGCGATGAACGTTTTCGACGGTACGCAGTCGGACAGCACGCAGGCACCGCCGGCCCCCTCGGCCTCCACCACGGTGACATCAGCGT
    < S  S  A  I  F  T  K  S  P  V  C  D  S  L  V  C  A  G  G  A  G  E  A  E  V  V  T  V  D  A  D
67803 CCAACTGGGCGGCGACCAGGGCCGCCTCGTACCCGGCCGGCCCCCCGCCGATGATCACGATCTGGCTCACAGCTATCGCCCCTCGTCCGT
    <  L  Q  A  A  V  L  A  A  E  Y  G  A  P  G  G  G  I  I  V  I  Q  S  V
67893 GCTCACAGTGACTTTCTTCTCCCCGACGCGTCCGACACGCACCGTCGTATTCTCCCCCAGCCGTCCGCCGGGCTATCGTCATCGCCGTGCG
                                                                                                > V  R
67984 TCACTACGCCGCCTACGGCTCAAACCTGGACCCCGCCCGGATGCGCGCCTACTGCCCGCACTCCCCGATGGTCGGCGTCGGCTGGCTGGAGG
    >  H  Y  A  A  Y  G  S  N  L  D  P  A  R  M  R  A  Y  C  P  H  S  P  M  V  G  V  G  W  L  E
68076 GCTGGCGGCTCACCTTCGCGGGTGAGGGCGCGATCGGCTGGGAGGGCGCGGTCAGCACCATCGTCGAGTCCCCCGGTGATCGGGTGTTCGTG
    >G  W  R  L  T  F  A  G  E  G  A  I  G  W  E  G  A  V  S  T  I  V  E  S  P  G  D  R  V  F  V
68168 GCGCTCTACGACATCCACCCGTACGACGCCGTCCAGCTCGACGAGATCGAGGGGGTGGCCTCCGGGACGTACCGCAAGCTGCACGTCCGCGT
    >  A  L  Y  D  I  H  P  Y  D  A  V  Q  L  D  E  I  E  G  V  A  S  G  T  Y  R  K  L  H  V  R  V
68260 CTCCACCCTCGACGGCGACGTGACCGCGTGGGTCTACGTCTTCGACGGGTACGAGGGCGGCCTGCCGACGGCGTGGTATCTGTCGGAGATCG
    >  S  T  L  D  G  D  V  T  A  W  V  Y  V  F  D  G  Y  E  G  G  L  P  T  A  W  Y  L  S  E  I
68352 CCAACGCCGCCGAGAAGGCGGGCGCGCCCGACGACTACGTCAGCGAGCTGCGGTCCCGCCCCACCGGCACGGCGTCGGCGTAGCGCGTCTC
    >A  N  A  A  E  K  A  G  A  P  D  D  Y  V  S  E  L  R  S  R  P  T  G  T  A  S  A  •
68443 CCACACTCCCAGTCTGCTCCGCCCGAGACGGGGCCGCACGGCGGCCCCCGCCGGGGGTCGTCTGTCACACATCATGGTCGCGCCCGTCACA
                                                                                                < •  V
68534 CCGCCGTGGCGGCGGGGACGGTGCGCTCGTACATGTCGGTCCAGCGCATCTCGCGCAGCCCCACCGAGCGGTAGAGCGTCGCCGGGGAGGTC
    <  A  T  A  A  P  V  T  R  E  Y  M  D  T  W  R  M  E  R  L  G  V  S  R  Y  L  T  A  P  S  T
68626 GGGTTGGTCAGGTCGACGCCGAGGCCGGCGTGCCGCCGTCCCTTCGCCGCGTAGACCGTGAAGGCCCGCCACAGCAGCGCGGCGCCGACCCC
    <P  N  T  L  D  V  G  L  G  A  H  R  R  G  K  A  A  Y  V  T  F  A  R  W  L  L  A  A  G  V  G
68718 GTGCCGCCGGTACTTCGGCAGCACCGACAGGGTCCGCACCCAGCCCGAGTCCTGTTCCAGCGCCTGGTCGGACGACTGCAACGCGCCGGCCG
    <  H  R  R  Y  K  P  L  V  S  L  T  R  V  W  G  S  D  Q  E  L  A  Q  D  S  S  Q  L  A  G  A  P
68810 GCTCCCCGTCGACCTCGGCGACGAACCACTCGTCCCAGGTCCTGTCGTACGCGGGCAGACGCTCCCGCCAGTGGTCGTACCCGGCCGGCTCG
    <  E  G  D  V  E  A  V  F  W  E  D  W  T  R  D  Y  A  P  L  R  E  R  W  H  D  Y  G  A  P  E
68902 TAGTCCGGGGTGTCCCGGAACGCCGTGTCGTAGATCCGGTGGAACAGGCGCAGGTCGTCCTCGTCGCCGGCGCGCAGCGGCCGGACCGTCAC
    <Y  D  P  T  D  R  F  A  T  D  Y  I  R  H  F  L  R  L  D  D  E  D  G  A  R  L  P  R  V  T  V
68994 CCCGGGTGGGGGCGGCGGCTCGGCGGGCAGCCCGGCCAGGTCACGACTCATCCGTACGTACCGCTTCACCCGGCTGAAACCGGCCTCGGTCA
    <  G  P  P  P  P  P  E  A  P  L  G  A  L  D  R  S  M  R  V  Y  R  K  V  R  S  F  G  A  E  T  L
69086 GCTCCGTCACCCAGCGGGTCTCCGGCGGGTAGGCCGAGGCGCGGACGGTCAGCGCGGGCAGGCTCCGCTCCGCGGCCCGCTCGGCGACCCGG
    <  E  T  V  W  R  T  E  P  P  Y  A  S  A  R  V  T  L  A  P  L  S  R  E  A  A  R  E  A  V  R
69178 TCCAGCATCAGAGCGAGCAGCGGGGCGCGTACCGCCTCGGCGCGCTCCGGGTCGACGAGGACGTCGACGAACTCCCGGCCCACCCCGGTCGG
    <D  L  M  L  A  L  L  P  A  R  V  A  E  A  R  E  P  D  V  L  V  D  V  F  E  R  G  V  G  T  P
69270 GTTGTCCACCACCGACCAGGCGACGAGCCGGCCCTGCGGGTCGCTGACCAGCCAGGAGTCGCGCGCCGGGTCGAAGAAGGGGGCCGTCAGGG
    <  N  D  V  V  S  W  A  V  L  R  G  Q  P  D  S  V  L  W  S  D  R  A  P  D  F  F  P  A  T  L  A
69362 CGGCCTTGACGTCTTCGGCGTCGAAGTCCGGGTGGCCGATCGCGAAGGTGTCTGCGGCGTGCACGACGGCGAGGATCCCAGGGACGTCGTCG
    <  A  K  V  D  E  A  D  F  D  P  H  G  I  A  F  T  D  A  A  H  V  V  A  L  I  G  P  V  D  D
69454 AGGGTGGGGCGGCGCGCCGCCCAGTCAGCGGGAAGAGTCACGGGGCGATCCTGGCAGCCACCCCGGTCCCGCGCCCCTCATTTTCAACCGC
    <L  T  P  R  R  A  A  W  D  A  P  L  T  V
69545 CCCGCGCCCTGCCCCCGCCGCCGCACGCGCTCGCCGGCGAGAGGGGACCCTTTCTACCCCAGGCGTTAGTAAGGGGCCCTTCCTTGCACCAC
                                                                                                < •  Y  P  A  R  G  Q  V  V
69637 GGCGCGTGCGGTGGTCAGCAGGTCGAGCAGCGCGGTGCCCTCGGCCGGCGTGAGCGCCCGGAATCCGGTCGACACCAGCCGGTCGGTCACCG
    <  A  R  A  T  T  L  L  D  L  L  A  T  G  E  A  P  T  L  A  R  F  G  T  S  V  L  R  D  T  V  A
69729 CCTCCGACCACAGCCGGCGGCGCACCAGCGGCCCGACCCGGGGGTACGGCGGCGGCCAGCCGCAGGCCAGCGCCCCGGCCTCCCCCTCCGGC
    <  E  S  W  L  R  R  R  V  L  P  G  V  R  P  Y  P  P  P  W  G  C  A  L  A  G  A  E  G  E  P
69821 CCGGCCAGCACCGCCTCCAGCGGCGTCATCCCGCCGGCCCGCACCGCCAGCAGGTACGCCCCGGCGAAGTGCTCCCGAAGCAGCAGCAGCCC
    <G  A  L  V  A  E  L  P  T  M  G  G  A  R  V  A  L  L  Y  A  G  A  F  H  E  R  L  L  L  L  G
69913 GGCGGCGGCACGGGCCCCCGGGGTGTCGTCCGGCGGCGGCACGGCCCGCCAGGCGGCAAAGAGTGGCATCCCGCTGGCGTCCGCGGCGTCGA
    <  A  A  A  R  A  G  P  T  D  D  P  P  P  V  A  R  W  A  A  F  L  P  M  G  S  A  D  A  A  D  V
70005 CCACCCGGTGCAGCAGCGTCGCCAGACGGATCACGCCGGGCACGGCGGTCAGGTCGCTCGCTGCCCCACCGGCAGCACTCGGCCAGGTTCGCC
    <  V  R  H  L  L  T  A  L  R  I  V  G  P  V  A  T  L  H  E  S  G  W  R  C  C  E  A  L  N  A
70097 GTGGCCACCTCCAGCGGAGCGTGCACGCGGGCGGCGGCGTCCCACCCGTCGGCGACCGCGTCGGGGGCGACGAAGCCGAGGGCCGCGCTCAC
    <T  A  V  E  L  P  A  H  V  R  A  A  A  D  W  G  D  A  V  A  D  P  A  V  F  G  L  A  A  S  V
70189 CGTGGCGGCCCCGACGTCGCCGAGCACCCCGGCCCGGCCGGCGATGTGGAAGGCCCAGCCGGAGATGCCCAGCAGACGGGCCCGGTGCAGGG
    <  T  A  A  G  V  D  G  L  V  G  A  R  G  A  I  H  F  A  W  G  S  I  G  L  L  R  A  R  H  L  T
70281 TGGCCGGGCAGCGGGCGAACATCTCCCCGAGCTCCAGCACCAACGGCTTGCTCGCGGCGGCGACCTGCTCCGGCGTCATCGGGTTCAGTCT
    <  A  P  C  R  A  F  M  E  G  L  E  L  V  L  P  K  S  A  A  A  V  Q  E  P  T  M     <  •  D
70372 GCCCCGCCGGGGCCTTCCGTGACAGCCCCGTCTTCGGCGTCGACCGCCTCGATCGCCCCCTCGATTTCGCCGGTGCGGCGCTGGGCGGCGGT
    <A  G  G  P  G  E  T  V  A  G  D  E  A  D  V  A  E  I  A  G  E  I  E  G  T  R  R  Q  A  A  T
70464 GACGGCCCGTTCCGCCGCCCGCCGGGCCAGCTTCCGCCGGCTGAGTTCCTGCTCGGCCTCTGCGCGCGATCGCTCCAGCTCGGCCAGCGACC
    <  V  A  R  E  A  A  R  R  A  L  K  R  R  S  L  E  Q  E  A  E  A  R  S  R  E  L  E  A  L  S  R
70556 GCTCGATGCCGGTCAGTTCCTCGGCACCGTCGTGCTCGGCCTCCACCGCGCCGGCCAGCTCCGCCTCGGCCCGCTCCTGGTCGGTACGCGCC
    <  E  I  G  T  L  E  E  A  G  D  H  E  A  E  V  A  G  A  L  E  A  E  A  R  E  Q  D  T  R  A
70648 CGCGCCAGTTCCCGTTCCAGCATCCGGCGTTGCCGGGCCCGCTCGGCACGGGCGGCGCGCTCGGCCTCCCGGGCGGCCCGCTTCGCGCGCGG
    <R  A  L  E  R  E  L  M  R  R  Q  R  A  R  E  A  R  A  A  R  E  A  E  R  A  A  R  K  A  R  P
70740 TGGTGGGTGGGTGGGCGGTGGCTGCTCCTCGCCGCCGGTGACCAAACGGAGCTGGGGGCGGGGCACCTCGCCGAAGCCGGCGTAGCTGGCGG
    <  P  P  H  T  P  P  P  Q  E  E  G  G  T  V  L  R  L  Q  P  R  P  V  E  G  F  G  A  Y  S  A  A
70832 CCCGCAGCAGCCGGCCGGAGCGCACCTGCCCGGCCACCTCCGTGTCGGAGAGCGCGGCGTCGAGCGTCGCCTCCACCTCGCCCAGCGGCAGC
    <  R  L  L  R  G  S  R  V  Q  G  A  V  E  T  D  S  L  A  A  D  L  T  A  E  V  E  G  L  P  L
70924 TTCCCGGCCGGCGGGCCGCCCTCGGCGTCGGCGGCCAGCCGGCGCGCCTCGGCGACCAGCGCGGCGACCGCCGCCCGCCGCTGGGCGGAGAG
    <K  G  A  P  P  G  G  E  A  D  A  A  L  R  R  A  E  A  V  L  A  A  V  A  A  R  R  Q  A  S  L
71016 TTCCCGCAGCCGGGGGCCGCGCAGGTCGCGCTGGGCGCGGCGCAGCGCCTCGGCGAGTTGGGTCAGGTCGGCGACCAGCTCGGGGCGGCGCA
    <  E  R  L  R  P  G  R  L  D  R  Q  A  R  R  L  A  E  A  L  Q  T  L  D  A  V  L  E  P  R  R  L
71108 GGGCGAGCAGGTTGACCAGCCACGCGGCCACGGTCGGGCGGCGCAGCCGGGCGATCTCGCGGGCCGTGGCCGGGTCGCCGGAGCGCCGGGCC
    <  A  L  L  N  V  L  W  A  A  V  T  P  R  R  L  R  A  I  E  R  A  T  A  P  D  G  S  R  R  A
71200 TCGGCGACGGCGGCGTCGCGGGTGGCGACGAACTTCTCCGGCGGCTCGGTGTAGAGCCGCCGGAGGAGGCTCTGCGGGGGCGGCACGGCTC
    <E  A  V  A  A  D  R  T  A  V  F  K  E  P  P  E  T  Y  L  R  R  L  L  S  Q  P  P  P  V     <  •
```

Figure 11S

```
71291 AGACGTCGAGCCGGCTGCCCGGCTCGAGGCGCTGGTAGTCGGTCCCCGACAGCGCGGCGTACTGACGGTTGAGGACGGCGAGGCCGTTGTCG
      <  V  D  L  R  S  G  P  E  L  R  Q  Y  D  T  G  S  L  A  A  Y  Q  R  N  L  V  A  L  G  N  D
71383 TTGAGCAGCCCGTCGTGCAGGGCGAAGGCTCGGCGCGGGGCGACCGCGCGGATGAAGTCGAGCACCTCGGAGAACTTCGACCAGGGGGCGTG
      <N  L  L  G  D  H  L  A  F  A  R  R  P  A  V  A  R  I  F  D  L  V  E  S  F  K  S  W  P  A  H
71475 GATCGGCGCGAAGAGGGTGTCCACGGGGGCGTCCTCGGGTGCCACCAGGGCGTCGCCGGGGTGGTAGACGACGTCGTTCAGCAGATACCCGA
      <  I  P  A  F  L  T  D  V  P  A  D  E  P  A  V  L  A  D  G  P  H  Y  V  V  D  N  L  L  Y  G  L
71567 GGTTGTCCACGACCGGGATGTCGGGATGGATGACGGCGTGCCGACCGCCGTACGCGCGCACCGCCACGCCCGCCGCGGTGAACGCCTGCCCG
      <  N  D  V  V  P  I  D  P  H  I  V  A  H  R  G  G  Y  A  R  V  A  V  G  A  A  T  F  A  Q  G
71659 GGTGAGATGGGCTCCAGGGCTTCGGCCACGTCGCCGAGGGCACCGGCCAGCGAGGCCGGGCCGTAGATGCGGAACGGCCAGCGGTCGAGCTG
      <P  S  I  P  E  L  A  E  A  V  D  G  L  A  G  A  L  S  A  P  G  Y  I  R  F  P  W  R  D  L  Q
71751 CCGGGTGAGAGCCGCGACGTCCACGTGGTCGGGGTGCTCATGGGTGATCAGCACCGCGTCCGCACCGTCCAGCGCGGTCGGGTCGCTGAAGA
      <  R  T  L  A  A  V  D  V  H  D  P  H  E  H  T  I  L  V  A  D  A  G  D  L  A  T  P  D  S  F  V
71843 CGCCCGGGTCGACGACCAGCACACCGCCGTCGTGCTCGACGCGGAGGCAGGAGTGGGCGAATTTGGTGAGCTGCATCGTGACTCCTCGAT
      <  G  P  D  V  V  L  V  G  G  D  H  E  V  R  L  C  S  H  A  F  K  T  L  Q  M
71933 TGACCCAATCGTGATGTCCCTCAGCGCAGTCTGCCGGAACCGGCGCGGTGCCGCGTCGCGTCTGAGGTATCGCCCGATGGGGCGTAGACGAT
72025 CGGAGCGGGAATGGACGGACACGCAAGACGCAGGTTGCTGACCGCGGTGGGGCTGGTGGCGCTGCTGGCGGCCGGTGGTTGCAGCGCCGACA
72117 GCGATGGGGCGGGAGAGCCTTCGGCGGCGGTGGCGCCCGAGCAGGCGGCACCTGCCGACGGGGGCAAGGCGGAGCAGGGTGCCGATGCCGGG
72209 GGAACGCGGTCCGGCGCGGGTGGCGGCTCACCGGACCTGCGGGTCGACCAGCGGTCAATCATCTACACCGGAACCATGCGGGTGCGGGTGG
                                                                                  >  M  R  V  R  V
72300 ACGATGTGGACGCCGCCGCCCGGTCCGCCATCACGGCGGTCACCGGCGTCGGCGGCTTCGTCGGCGGCGACGAGCGCAGCAGCGGCGGAACC
      >D  D  V  D  A  A  A  R  S  A  I  T  A  V  T  G  V  G  G  F  V  G  G  D  E  R  S  S  G  G  T
72392 GCCGACGCCCGGGCGGAGTTGCAACTGCGGGTGCCGGCGGAGCGGTTCACGGCCGTCCTGGAGGAGTTGGCGAGGCTCGGCCGGCAGGAGCA
      >  A  D  A  R  A  E  L  Q  L  R  V  P  A  E  R  F  T  A  V  L  E  E  L  A  R  L  G  R  Q  E  Q
72484 GCGGGCGATCCGCACGGAGGACGTGACCGAGGAGACCGTGGATCTCGACGCGCGGATCGCCACCCAACGGGCCCGGGTCGAGAGCGGTCGCA
      >  R  A  I  R  T  E  D  V  T  E  E  T  V  D  L  D  A  R  I  A  T  Q  R  A  R  V  E  S  G  R
72576 AGCTGCTGGCGCGGGCCACCTCGATCGGCGACCTGGTGACGCTGGAGAGCGAGGTGGCTAGGCGGGAGGCCGACCTCGCCTCGCTGGAGGCG
      >K  L  L  A  R  A  T  S  I  G  D  L  V  T  L  E  S  E  V  A  R  R  E  A  D  L  A  S  L  E  A
72668 AAGAAGCGCCGGCTGGCCGACCTGACCTCGCTCTCCACCATCACCCTCACCCTGGTCGGTCCGGAGGCGGAGGCCCGGGACACCGAGCCCGA
      >  K  K  R  R  L  A  D  L  T  S  L  S  T  I  T  L  T  L  V  G  P  E  A  E  A  R  D  T  E  P  D
72760 CACCGGCTTCGTGGTCGGCCTGCGCGGCGGCTGGACGGCGTTCGTCGCCTCGCTGGGCGTGCTGCTCACCGTGCTCGGGGCGCTGCTGCCGT
      >  T  G  F  V  V  G  L  R  G  G  W  T  A  F  V  A  S  L  G  V  L  L  T  V  L  G  A  L  L  P
72852 TCGCGGTGGCCCTCGGCGTGCCGGTGGCGGTGCTGCTTGCGGTGCTGCGGCGGCGCCGGCGTCGACCGCCGGCGCCGGCCGTCAACGCGCC
      >F  A  V  A  L  G  V  P  V  A  V  L  L  A  V  L  R  R  R  R  R  R  P  P  A  P  A  V  N  A  P
                                                                                  <  ∘  R  A
72943 GCCGCCAGTGCCCGCAGCGCGGTCTGCACCATGACCCGGATGCCGACCGCGATGGCCCCCTCGTCGACGTCGAACGAGGCCCGGTGCAGGT
      >  P  P  V  P  A  A  R  S  A  P  ∘
      <A  A  L  A  R  L  A  T  Q  V  M  V  R  I  G  V  A  I  A  G  E  D  V  D  F  S  A  R  H  L  D
73034 CGACGTTCGGGCCGGACCGGCCGACGCCGAGGCGGGCCAGCGCGCCGGGGACGTACTCCAGGTACCAGGAGAAGTCCTCGCCGCCCATGCTC
      <  V  N  P  G  S  R  G  V  G  L  R  A  L  A  G  P  V  Y  E  L  Y  W  S  F  D  E  G  G  M  S
73126 TGCGGGGTCTCCGCGACCCCCTCCGGGCCGAGCGCGGCGTGGGTCGCCGCCGTGAGCACCTGGATCGCCCGGGCGTCGTTGGTCACCGGCGG
      <Q  P  T  E  A  V  G  E  P  G  L  A  A  H  T  A  A  T  L  V  Q  I  A  R  A  D  N  T  V  P  P
73218 CCGGCCGCGTAGGTACTCCAGGTCGACGGTGGCGCCGGTGGGGGCGATGACGTCCCGCACCACCTGAGCGACGATCTTGGGGGCCTGGTCCC
      <  R  G  R  L  Y  E  L  D  V  T  A  G  T  P  A  I  V  D  R  V  V  Q  A  V  I  K  P  A  Q  D  W
73310 AGGTGTCGCGGTCCATCACCCGCAGGGTGCCGGACGCGGACGCCTCGGACGGGATCACGTTGTACCGGGTGCCGGCCGAGGCGTGGCCGAAC
      <  T  D  R  D  M  V  R  L  T  G  S  A  S  A  E  S  P  I  V  N  Y  R  T  G  A  S  A  H  G  F
73402 ACGAGCAGCAGCCCGCTGTTGGCCGGCACCCGGCGGCTGACCAGGGCTGGCACCTCGGTGACCAGCCGGCCGAGCGCGTCGACCAGGTCGAC
      <V  L  L  L  G  S  N  A  P  V  R  R  S  V  L  A  P  V  E  T  V  L  R  G  L  A  D  V  L  D  V
73494 GGTCAGGTGCGGGCGAGCGGTGTGCCCGCCGGGGCCGGTGAGCCGGACGGTGACGTTGTCGGCGGCGGCGGTGATCGGGCCGACCCGCAGGC
      <  T  L  H  P  R  A  T  H  G  G  P  G  T  L  R  V  T  V  N  D  A  A  A  T  I  P  G  V  R  L  G
73586 CGACCTTGCCGACGGGCTGGTTGGGGTCGCAGTGCAGTGCGAAGATCTGCACGACGTCGTCGAGACCGCCGGCCTCGATGACCTCCAGCGAG
      <  V  K  G  V  P  Q  N  P  D  C  H  L  A  F  I  Q  V  V  D  D  L  G  G  A  E  I  V  E  L  S
73678 CCGCAGGGCAGGATCTCCTCGGCCGGCTGGAAGATCAGCCGGACCCGGCCGTCCAATTCGCCGAGGTTGGCGAGTTGGGCCAGCAGCACGCC
      <G  C  P  L  I  E  E  A  P  Q  F  I  L  R  V  R  G  D  L  E  G  L  N  A  L  Q  A  L  L  V  G
73770 GACGCCGAGCAGCACGGTGGTGTGCACGTCGTGGCCGCAGGCGTGGCAGACACCGTCCTTGGTGGACCGGTAGGGCACGTCCTTGACGTCGG
      <  V  G  L  L  V  T  T  H  V  D  H  G  C  A  H  C  V  G  D  K  T  S  R  Y  P  V  D  K  V  D  T
73862 TCAGCGGCAGCGCGTCGATGTCGGCGCGGAGCGCGACCACCGGGCCGTCGGGGCGGCCGTCGATGTCGCAGATGACCCCGTTGCCCTTTGGC
      <  L  P  L  A  D  I  D  A  R  L  A  V  V  P  G  D  P  R  G  D  I  D  C  I  V  G  N  G  K  P
73954 AGCAGGCGCGGGCGCAACCCGGCGAGCGACAGCTCGCGGGCGATCAGGGCCGCCGTCTCGAACTCCTCGCCGGAGAGCTCCGGGTGGGAGTG
      <L  L  R  P  R  L  G  A  L  S  L  E  R  A  I  L  A  A  T  E  F  E  E  G  S  L  E  P  H  S  H
74046 GATGTGCCGGCGGGTGGCGATAAGGCCGGGCATCCGGAGGGCGAGCAGATGGTCGAGCTCGAAGGGCAAAGGCTGCGACCCGGACGGCGACT
      <  I  H  R  R  T  A  I  L  G  P  M  R  L  A  L  L  H  D  L  E  F  P  L  P  Q  S  G  S  P  S  E
74138 CCGGCCAGGCCGACGACGCCAGGTGGCTGCCGTTCGGCAGCGTCAACGCACTCGTCACGTCGAAATCTCGATCACTAGAAACGGATGGATC
      <  P  W  A  S  S  A  L  H  S  G  N  P  L  T  L  A  S  T  V
74229 ATCAGGGATGACAGCCGCCAGCCTAGACCTTCGACGGTGACTCTGTGCAACATCATTCCCGTAGCGATCGGACCGCGCAGCGTCACGAATAC
74321 CCTGGTGGAAGGGCTCCATAATCTGCGGGACAGCAGGTAGATCGCGGTTGAACGCCGTCATCTGCCCCCCACCTCCTACAACCCGTAACCGA
74413 TTCGGCGGTCACGAAATCACCGTCGATCCGGGGCCGTCGCTACCGAATTGTCGCATTAGTCGTCTCGGTTAACTGCCGCTCGGACAAGTAAC
74505 CGACCGCACTCGGCAGTCGGACGACTCCCGACGGTGACACGACGGGCCGACCTGCTCCCGCACATGCTGTCCGTCCCAATCACCCGGACGGG
74597 TTACCCACTGCCCCGGGTGGCACACACCGGGCTGCCCCGGGTGGCACACACCAGGCGACCGTAGCCCCGAACGGTTACGCCCCGCGACCC
74689 CTCATCCGAGACAAGGGGTCAGAACCGGTCGCTGGGGCGGTACGTCCCCCACACCTGGCGCAGGGTGCCACAGACCTCGCCCACCGTGGCC
                  <  ∘  F  R  D  S  P  R  Y  T  G  W  V  Q  R  L  T  G  C  V  E  G  V  T  A
74780 CGGGCCCGCAGCGCCTCCTTCATCGGGTGCAGCACGTTCGCCGTACCCTCGGCGGCGGCCCGCAGCTCACCCAGCGCGCGCTCGACGGCGTC
      <R  A  R  L  A  E  K  M  P  H  L  V  N  A  T  G  E  A  A  A  R  L  E  G  L  A  R  E  V  A  D
74872 GCTGTCGCGCTCCACTCGCAGCTTGGCCAGCCGCTCGGCCTGGGCAGCCTCGATCGTCGGGTCCACCCGCAGCGGCTCGTACGGCTCGTCGG
      <  S  D  R  E  V  R  L  K  A  L  R  E  A  Q  A  A  E  I  T  P  D  V  R  L  P  E  Y  P  E  D  A
74964 CGTCGACCGTGAACCGGTTGAGGCCGACCACCACCCGCTCGCCCGAGTCGATCTCCTGGGCGATCCGGTACGCGGACTGCTCGATCTCCCGC
      <  D  V  T  F  R  N  L  G  V  V  V  R  E  G  S  D  I  E  Q  A  I  R  Y  A  S  Q  E  I  E  R
75056 TTCTGGAAGCCCGCCTCGATGGCGTCGACCACCGAGCCGTGGTCGGCCACCCGCTCCATCAGCTCCACCACCGCCGCCTCGATCTCGGCGGT
      <K  Q  F  G  A  E  I  A  D  V  V  S  G  H  D  A  V  R  E  M  L  E  V  V  A  A  E  I  E  A  T
```

Figure 11T

```
75148 CATCGCCTCCACCACGTACGACCCGGCGAACGGGTCGACGGTGGCGGTCAGGTCCGTCTCGTACGCGAGCACCTGCTGGGTGCGCAGCGCCA
     < M  A  E  V  V  Y  S  G  A  F  P  D  V  T  A  T  L  D  T  E  Y  A  L  V  Q  Q  T  R  L  A  L
75240 GCCGGGCGGCCTTCTCGGTGGGCAGCGCGATGGCCTCGTCGAAGCTGTTCGTGTGTAGCGACTGGGTGCCGCCGAGCACCGCGCCCAGCCCC
     < R  A  A  K  E  T  P  L  A  I  A  E  D  F  S  N  T  H  L  S  Q  T  G  G  L  V  A  G  L  G
75332 TGGATCGCCACCCGGACCAGGTTCACCTCGGGCTGCTGGGCGGTGAGCTGCACGCCCGCCGTCTGGGTGTGGAAGCGCAGCATCATCGACTT
     <Q  I  A  V  R  V  L  N  V  E  P  Q  Q  A  T  L  Q  V  G  A  T  Q  T  H  F  R  L  M  M  S  K
75424 CGGGTTCTTCGCGCCGAACTCGTCGCGCATCAGCCGGGCCCAGATCCGCCGGGCGGCACGGAACTTCGCGACCTCCTCCAGCAGGGTGGTCC
     < P  N  K  A  G  F  E  D  R  M  L  R  A  W  I  R  R  A  A  R  F  K  A  V  E  E  L  L  T  T  R
75516 GGGCGACGAAGAAGAACGACAGCCGGGGCGCGAAGTCGTCCACCGCCAGCCCGGCGGCGAGCGCGGCCCGGACGTACTCGACGCCGTTGGCC
     < A  V  F  F  F  S  L  R  P  A  F  D  D  V  A  L  G  A  A  L  A  A  R  V  Y  E  V  G  N  A
75608 AGCGTGAACGCGATCTCCTGCGCGGGCGACGCGCCGGCCTCGGCCATGTGGTAGCCGGAGATGGAGATGGTGTTCCACTTCGGCACCTCCGC
     <L  T  F  A  I  E  Q  A  P  S  A  G  A  E  A  M  H  Y  G  S  I  S  I  T  N  W  K  P  V  E  A
75700 CCGGCAGTAGGCGAACGTGTCGGCGACCAGCCGCAGCGAGGGCTTCGGCGGGAAGATGTACGTGCCCCGGGCGATGTACTCCTTGAGGATGT
     < R  C  Y  A  F  T  D  A  V  L  R  L  S  P  K  P  P  F  I  Y  T  G  R  A  I  Y  E  K  L  I  D
75792 CGTTCTGGATGGTGCCGTTGAGCGCCGCGCCCGGCACCCCCGCCTCCTCGGCGACGAGCTGGTAGAGCAGCAGCAGCACCGACCCCGGGGCG
     < N  Q  I  T  G  N  L  A  A  G  P  V  G  A  E  E  A  V  L  Q  Y  L  L  L  L  V  S  G  P  A
75884 TTGATCGTCATCGAGGTGGAAACCTTGTCCAACGGGATGCCGTGGAACAGCAGCCGCATGTCCTCGATCGAGTCGATGGCGACGCCGACCTT
     <N  I  T  M  S  T  S  V  K  D  L  P  I  G  H  F  L  L  R  M  D  E  I  S  D  I  A  V  G  V  K
75976 GCCGACCTCGCCGTGGGCGATCGGGTCGTCCGAGTCGTACCCCATCTGGGTGGGCAGATCAAAAGCGACGGAGAGGCCCATGGTGCCGGCGC
     < G  V  E  G  H  A  I  P  D  D  S  D  Y  G  M  Q  T  P  L  D  F  A  V  S  L  G  M  T  G  A  R
76068 GCAGGAGCTGGTGGTAGCGCGCGTTGCTCTCCGTCGCGGTGCCGAAGCCGGCGTACTGGCGCATCGTCCACGGCCGCGAGGTGTACATGGTG
     < L  L  Q  H  Y  R  A  N  S  E  T  A  T  G  F  G  A  Y  Q  R  M  T  W  P  R  S  T  Y  M  T
76160 GAGTAGACCCCACGGGTGTACGGGAACTCCCCCGGCTCGCCCAGCCGCTCGGGCAGACCCTCCGGCAGGTCCCTCTGGGTGTAGACACCCTT
     <S  Y  V  G  R  T  Y  P  P  F  E  G  P  E  G  L  R  E  P  L  G  E  P  L  D  R  Q  T  Y  V  G  K
76252 GATCGGGAAGCCGGACTCGCTCGACCGCGGTTCACTCATCCCCGGATGGTAGGACGTGCCACCGCGCCGGAGGGTGAGGGATTGCGCACAT
     < I  P  F  G  S  E  S  S  R  P  E  S  M
76343 CGCACCCCTGTCTTTCCCCGCCGACTCCGAGGGTGAACACCTGGCCACGTTCGCTCCGATTAGGTAAACGTTCCGCCGCGTCGGGTTTCGCA
76435 TCGGGCGTCGGAACCAGCAAGATAGAGGAGTTGTGTCCCAGCCCCCTCGATTTCCCCCGGTGGCTCTTCTGTGACTCAGATCCCGACGTGGA
76527 GCGGCGGACCAGTCAGCCCACCCCACGGACGTGCGGCAGCCGGCACCACCATCGGTGACCGGTACTCGCTCCGGTCCGCGGTGGGCAATGGC
76619 GGCATGGGCACGGTCTGGCGTGCCACAGACACCCTGCTGCGGCGCGACGTGGCGGTGAAGGAGGTCGTCCTCCCGCCCGGCCTCGCCCCGA
       > M  G  T  V  W  R  A  T  D  T  L  L  R  R  D  V  A  V  K  E  V  V  L  P  P  G  L  A  P
76710 GCGACCGCGACGCCATGTACGAACGCACGCTGCGCGAGGCCCGCGCGGCGGCGGCCATCCAGCACCCGGCCGTGGTCCAGGTGTACGACGTG
     >S  D  R  D  A  M  Y  E  R  T  L  R  E  A  R  A  A  A  A  I  Q  H  P  A  V  V  Q  V  Y  D  V
76802 GTCACCGAGGGTGGTCGCCCCTGGATCGTGATGGAGCTGCTGGACGCCCGCAGCCTGGCCGACATGGTGATCGAGGACGGGCCGGTGGCCCC
     > V  T  E  G  G  R  P  W  I  V  M  E  L  L  D  A  R  S  L  A  D  M  V  I  E  D  G  P  V  A  P
76894 CCGCGCGGTCGCCAAGATCGGCATCGCCCTGCTCGGCGCGCTGGAGGTGGCCCACGCGATCGGGGTGCTGCACCGCGACGTGAAGCCGGCCA
     > R  A  V  A  K  I  G  I  A  L  L  G  A  L  E  V  A  H  A  I  G  V  L  H  R  D  V  K  P  A
76986 ACGTGCTGATCTGCACCGACGGCCGGTGCGTGCTGACCGACTTCGGGGTGGCCAAGCTCCCCACCGACGTGCAGCTCACCACGCCGGGGATG
     >N  V  L  I  C  T  D  G  R  C  V  L  T  D  F  G  V  A  K  L  P  T  D  V  Q  L  T  T  P  G  M
77078 GTGCTCGGCTCGCCGCACTTCATCTCCCCCGAGCGGGCCATGGGCCAGGAGTTCGGCCCGCCGAGCGACCTGTTCTCCCTCGGCGTCACGCT
     > V  L  G  S  P  H  F  I  S  P  E  R  A  M  G  Q  E  F  G  P  P  S  D  L  F  S  L  G  V  T  L
77170 CTACACGGCGGTGGAGGGCCGGCCCCCGTTCGACAGGGGCGACCCGATCGAGACCATGCACGCCGTGGTCGAGGACCCGCCGGCCACGCCGC
     > Y  T  A  V  E  G  R  P  P  F  D  R  G  D  P  I  E  T  M  H  A  V  V  E  D  P  P  A  T  P
77262 AGCGCAGCGGCCCGCTGACCCGGGTGCTGATGGGGCTGCTGGAGAAGGACCCGGCCCGCCGCCTCGACGTGCACACCGCCCGCGCGATGCTC
     >Q  R  S  G  P  L  T  R  V  L  M  G  L  L  E  K  D  P  A  R  R  L  D  V  H  T  A  R  A  M  L
77354 CGCGAGCTGCTCGCCGGCCCGCTGACCAGCACCGCCACCGCCGTCAACTCGGTCACCGACCCGTACGCGGTGGTGCCGGTCAAGCAGCGCCC
     > R  E  L  L  A  G  P  L  T  S  T  A  T  A  V  N  S  V  T  D  P  Y  A  V  V  P  V  K  Q  R  P
77446 GGCCGTCGCCCCACCGCCCTCCGCTGCGGAGCCGAAGCCGAGCGGGCAGATCGGCGGCCGGGCGATGCTCGCCCCCGGCGAGTCGCTGACCG
     > A  V  A  P  P  P  S  A  A  E  P  K  P  S  G  Q  I  G  G  R  A  M  L  A  P  G  E  S  L  T
77538 ACCGGCTGGCGGCCCTGCGCCGGGGCGAGAAGACGAGGAAGAGGAAGACGACGACCGCCGCCGCGCTGGACGACACCAGCGCCGACGCGCTT
     >D  R  L  A  A  L  R  R  G  E  K  T  R  K  R  K  T  T  T  A  A  A  L  D  D  T  S  A  D  A  L
77630 GCCGGCCCGCTGCACACCCCCACCGGGGCGATGCCCGCGCCCCCGCCCGCCGGCCGGACGTACGGCGGTTCGTCGGAGGCCACCCAGCGGGT
     > A  G  P  L  H  T  P  T  G  A  M  P  A  P  P  P  A  G  R  T  Y  G  G  S  S  E  A  T  Q  R  V
77722 CGACGCGGGGACCGCGCCGGAGGCCACCCAGCGGATGACGTACGGCAGCCCGCCCGACGCCACCCAGCGGGTGTCCCACGGGAGCGGCCCGT
     > D  A  G  T  A  P  E  A  T  Q  R  M  T  Y  G  S  P  P  D  A  T  Q  R  V  S  H  G  S  G  P
77814 CGGAGGCCACCCAGCGGGTGCCCTACGGCGGCGGCTCGGCGGACGCCACCCAGCAGGTGCCCTTCGGTCGCCGGCCCGACGCGACGCAGCGG
     >S  E  A  T  Q  R  V  P  Y  G  G  G  S  A  D  A  T  Q  Q  V  P  F  G  R  R  P  D  A  T  Q  R
77906 GTCCCCTACGGCAGCCAGCCCGGCGCGACGCAGCCGGTCCCCGGCTTCGGCGCGTCGCCGGACGCCACCCAGCGGGTCGGCGGGGCGTACGG
     > V  P  Y  G  S  Q  P  G  A  T  Q  P  V  P  G  F  G  A  S  P  D  A  T  Q  R  V  G  G  A  Y  G
77998 CGGCGGCCAGTGGTCGGTGCCCGGCACCGGCCAGCCGTGGGCCACCCCGGCCACCGCGCCCGCCCCGGCCACCGCCGGCGGCGGCGGGGTCG
     > G  G  Q  W  S  V  P  G  T  G  Q  P  W  A  T  P  A  T  A  P  A  P  A  T  A  G  G  G  G  V
78090 GCCGCCTCGTCGCCACGGTCAAGGGCTGGCCGCGCAAGGTGCAGCTCGCCGCGGCCGGCGGCGTCGCCGTGCTGCTGCTGATCGGCGTGTTC
     >G  R  L  V  A  T  V  K  G  W  P  R  K  V  Q  L  A  A  A  A  G  G  V  A  V  L  L  L  I  G  V  F
78182 GCCCTCTTCGGCGGCGACGACCCGGAGCAGCCGACCACCCCGCAGGGGCAGCCGAGCGCCGGGGCGCCCGCCGGCCCCGGGGTGGAGATGCA
     > A  L  F  G  G  D  D  P  E  Q  P  T  T  P  Q  G  Q  P  S  A  G  A  P  A  G  P  G  V  E  M  Q
78274 GGAGCAGTCGGCCAAGGGCGTCACGGTGCAGGTGCCCAAGGGCTGGGAGCGGCGCAGTGCCGACGGGGGCGTGTGGGTCGACTACATCGATC
     > E  Q  S  A  K  G  V  T  V  Q  V  P  K  G  W  E  R  R  S  A  D  G  G  V  W  V  D  Y  I  D
78366 CGGAGGACAACAGCCGCAAGGTGCGCATCCTCGCCGAGCGGTGGAGCGGCACGTCGACGCGCTGGGCCGAGACCGCCGCGAACGGGCTGCGG
     >P  E  D  N  S  R  K  V  R  I  L  A  E  R  W  S  G  T  S  T  R  W  A  E  T  A  A  N  G  L  R
78458 ACCCGGTCGGCCTCCTGCCAGAAGCCGTACAACCAGGTGTCGATGACCGAGCAGGAGCTCGACGGCAAGGCGGCGGCCGAGTTCGAGTACAC
     > T  R  S  A  S  C  Q  K  P  Y  N  Q  V  S  M  T  E  Q  E  L  D  G  K  A  A  A  E  F  E  Y  T
78550 CTGCGGCGACGGCGAGGGCAAGCGGCACGGCGTGTGGCGCGGGGTGGTGCACGAGGGCAAGGTCTACTCGTTCTACCTCTCCTCGACCGACG
     > C  G  D  G  E  G  K  R  H  G  V  W  R  G  V  V  H  E  G  K  V  Y  S  F  Y  L  S  S  T  D
78642 CCCGCTTCGCCGAGAGCAAGCCGATCTTCGATCAGATGGTGGCGTCGTTCAAGCTCCGCGGGAGCGACTGAGCCGGGCCGGGGGCCGACGC
     >A  R  F  A  E  S  K  P  I  F  D  Q  M  V  A  S  F  K  L  R  G  S  D  •
78733 GACGCCGGCCGGGCGGGCCGACGCGACGTGGTGAGCCGCCGCCGTGCTATCAAGAGCCATGGCGGCGGACACCACTGACCTCGACGACACG
                                                                 > M  A  A  D  T  T  D  L  D  D  T
78824 CGCGATCTGGACGACCTTCGCGACCGGGCCCGGCGGTGGCTCGACGACGACCCCGACCCGGCCACCCGCGACGAGCTGGAGGCCGTGCTCGA
     > R  D  L  D  D  L  R  D  R  A  R  R  W  L  D  D  D  P  D  P  A  T  R  D  E  L  E  A  V  L  D
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Figure 11U

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78916 CGGGCTGCCGGCGAGCGCGGCCGAGCTGGCCGACCGGTTCGCCGGGCCACTGACCTTCGGCACCGCCGGGCTGCGCGGCCCGCTGCGCGCCG
      > G L P A S A A E L A D R F A G P L T F G T A G L R G P L R A
79008 GCCCCAACGGGATGAACCTCGCCGTGGTCACCCAGGCCGCCGCCGGGCTCGTCGCCTGGCTCGCCGCCCAGGACGCCACCGGGCCGCTGGTC
      >G P N G M N L A V V T Q A A A G L V A W L A A Q D A T G P L V
79100 ATCGGGTACGACGCCCGGCACGGCTCGCGGGAGTTCGCCGAGCGCACCGCCCAGGTGGCCACCGGCGCGGGCCGCCCGGCGCTGCTGCTGCC
      > I G Y D A R H G S R E F A E R T A Q V A T G A G R P A L L L P
79192 CCGCCCGCTGCCCACCCCCGTGCTGGCGTACGCGGTGCGGCAGCTCGACGCGGCGGCCGGCGTGATGGTGACCGCCAGCCACAACCCGCCCC
      > R P L P T P V L A Y A V R Q L D A A A G V M V T A S H N P P
79284 AGGACAACGGCTACAAGGTCTACCTCGGCGCGCAGCTCGGCGGCGAGCTGGGCGCGGGGGCGCAGATCGTGCCGCCGGCCGACACCGGCATC
      >Q D N G Y K V Y L G A Q L G G E L G A G A Q I V P P A D T G I
79376 GAGGCCGCCATCCGGGCGGTCGGCCCGCTGGCCGACGTACCGCTGGGCCCGGCCGGGCAGGTCGTCGGCGACGACGTGGTCGTGTCGTACGT
      > E A A I R A V G P L A D V P L G P A G Q V V G D D V V V S Y V
79468 CGACCGGGCCGCCGCCGTGGTCGACCCGGCGGGGCCCCGGAGCCTGAAGGTGGCCTACACGCCGCTGCACGGCGTGGGCGCGGCCGTGCTGA
      > D R A A A V V D P A G P R S L K V A Y T P L H G V G A A V L
79560 CCGCCGCCTTCGCCCGCGCCGGCTTCGGCATCCCCGGCGTGGTGCCCGAGCAGGCGGTGCCGGACCCGGACTTCCGGACCGTCAGCTTCCCC
      >T A A F A R A G F G I P G V V P E Q A V P D P D F R T V S F P
79652 AACCCGGAGGAGCCGGGGGCGGTGGACCTCCTCGTCGCGCTCGCCGAGCGCACCGGGGCGGACCTGGCGATCGCCAACGACCCCGACGCGGA
      > N P E E P G A V D L L V A L A E R T G A D L A I A N D P D A D
79744 CCGCTGCGCGGTGGCCGTCCGCGACGGCCGGGCGGCGGGCCCGGCACCGGTGAGTGGGGGCGCCTGGCGGATGCTGCGCGGGGACGAGGTGG
      > R C A V A V R D G R A A G P A P V S G G A W R M L R G D E V
79836 GGGCGCTGCTCGCCGACCATCTCATGCGCCGTGGCGTCCACGGCCTGTACGCCACCACCATCGTGTCGTCGTCCCTGCTACGGGCCATGTGC
      >G A L L A D H L M R R G V H G L Y A T T I V S S S L L R A M C
79928 GCCGCCCGTGGCCTGCCGTACGACGAGACGCTGACCGGCTTCAAGTGGATCGTCCGGGCCGGCGGCGGACCGCTGGGTGAGGCCGGCTCCGA
      > A A R G L P Y D E T L T G F K W I V R A G G G P L G E A G S D
80020 CCCGCTGGTCTTCGGCTACGAGGAGGCGCTGGGCTACTGCGTCGCCCCGGAGCACGTCCGCGACAAGGACGGCATCACCGCCGCGCTGACCG
      > P L V F G Y E E A L G Y C V A P E H V R D K D G I T A A L T
80112 TCGCCGAGCTGGCCGCCGGGCTGAAGGCGCAGGGGCGCACCCTCACCGACCGGCTCGACGAGCTGGCCGCCGAGTTCGGCGTGCACCACACC
      >V A E L A A G L K A Q G R T L T D R L D E L A A E F G V H H T
80204 GACCAACTCTCGGTGCGGGTGGACGACCTGCGCATCATCGCCGACGCGATGGCCCGGGTCCGGGCGGCCACCCCGACGACCCTGCTCGGCCG
      > D Q L S V R V D D L R I I A D A M A R V R A A T P T T L L G R
80296 CCCGGTGACCGAGGCGCGGGACCTGCTCCCCGAGGCGGACGTGGTGATCCTGCGTACCGACGGGGCACGGGTGGTGATCCGCCCGTCGGGCA
      > P V T E A R D L L P E A D V V I L R T D G A R V V I R P S G
80388 CCGAGCCGAAGCTCAAGGCGTACCTGGAGGTGGTGGAGCCGGTGGCGGACGGCGACGTGCCGGCGGCCCGGACGCGCGCGGCGGCCACGCTG
      >T E P K L K A Y L E V V E P V A D G D V P A A R T R A A A T L
80480 GCGGCACTCCGCACGGAAATCGCCGCCCTGGTGCAGGGATGAGGTGTGCTCCCGCTTCCGACGCTCTCTCAGCGGGTTGGCGTGTCGCCCC
      > A A L R T E I A A L V Q G •
80571 CAGGTTCGTGGTGATATGCGGCCAGGTAAGCCACCGTCCTGCCACTATCCATGTCGTAGAACATGATGCGTGCCACTTGGATGTAGTAGTAG
80663 GTGACCAATGAGGTGAACCCGGGGCCCTGTTTGAGCGTGTACGTAGCGCCGAAGCCACTGGCAGTCACATCGTCACGGCGGGCTTTCCCGTT
80755 AGCGCTCGCGTAGCTCAGCGCAGCAGGAACATCCTCCCCGCCATAGGGATACAGCAGCTGGCTGGTGTATCCCTTCTCGAAGGGCTTTGCAG
80847 GTTCTGCCGGCAAGGGCGAGAGGTCCTGGGCGTCCGTCTTGATCACGATCTCGTAGAGCCGGACATCGGCCGTCTCGGTGTTGTACGCCAGG
80939 ATGACCGGCACCGGCAAGGTGTTTGGGAGCGTGACCGAAATGGACGTGAACCCGGGTCCGGGGCGCTGCGTCGGCCGCTGCCCGGCTTGGGT
81031 GGCGGGCCCGTCCGAGGAATAACTACGGAACATGCAACTGCCGTCTGTCTTGTTGTACAGGAACAGCCACTGCCGCTTTCCACCCTCGCCGT
81123 TCACCTCGAAGGGCGCTACGGACGACCATCCAGCGCCCCAGTTGTCCTTCTGGCCATCAGGCGGCCACACCTGCTCGCAACCGTCTTCGTTG
81215 TCCACAACCTGCCACACGGCGCTGTTGCCGGTAAGGGCATCGTAGAGCTGGACATACCGCCTGTCGTTCTGCACGACGGGAACGACGGAGGT
81307 CCACCCCTTCCCGAAATTGCGCTGCCAGCGGGGAGGCCACTCGGGTGGCATCTCGTCGTGGGCATTGACTGGACCGAAGGCGGCCGTGCCGT
81399 CATTGCTGTTGTAGAACAGCACCGCTGGGCCACTGTAGTGCCCGTCGAAATGCAGAGATATGACGTGCGTGAACCCTGGTCCGAGTTGGACA
81491 TCATAGAGAGCATTCCGGAGTGACATGGGTTTACCCCGTCCTAGGGATCACTGCTTCTCAACAAGATCATCAACGGTGTGCGGCAGGCTGCA
81583 CAATCGGGTGGAAGAAGAGCCAGCACCGGGCCTCACTGGCCATCACAGTATCGTCTGACCTCTTCGACCGGGCCCGAAACGGGCGAACCGAG
81675 AGCGTTCCGCGCATCTGTCGGTCGGGCGTGTCGAAGGTGCGGCTGTTCGCCACGTGCGCGGCGAGCAGGGTGCCCTCCGCGCCGTCACGGGT
81767 TCTGCCACGAGGCGGCCAGGACCCAGACGGTGACCAGCCGGCCCAGGGTGCCGGTCACGATGAACCGCTTGCGACCGCTGGCTGCGCCGCTC
81859 CGGCGGCCCTCCGCGCCGGACCGGGAACGCGGCACGCTCACCCCGCGTGATCCCTTGCCCACGAAGGGCTCGTCTGAATAGCATCAGCACAT
81951 CAGGCCCCACCATTACCCGGCACCATTGGCATTCGCTTTCTTCGACGTTGCGGCTGCGGTGCCCGGGCGTTGCATTTCCGGCGGAAAGGTGT
82043 TGCACGGTGCGTGAAACAAATGGCTCGACCGTGCCGCGACGGCAGCTCGGCAGGCTGCTCACCCAGCTCCGCGAGAGCGCCCATATCAGCA
                                                    > V P R R Q L G R L L T Q L R E S A H I S
82134 TCGACGCGGCGGCCGGCGAGCTGGACTGCTCGCGGCAGAAGCTCTGGCGGATCGAGCGGGGGCTGACCTCGGCCAAGACACCGGACGTCCGG
      >I D A A A G E L D C S R Q K L W R I E R G L T S A K T P D V R
82226 GTGCTCTGCGAGCTGTACCGGGCCACGCCCGACCAGGCGAGCGTGCTGCTCGGGCTCGCCGAGGTGAGCCGGGCCGAGGGGTGGTGGCACGC
      > V L C E L Y R A T P D Q A S V L L G L A E V S R A E G W W H A
82318 CCACGGCAGCTCCGTGCCGGCCTGGTTCTCGCTCTACGTCGGCCTGGAGAACGTCGCGAGCAGCATTCGGCACTACAACGCGGAGCTGGTGC
      > H G S S V P A W F S L Y V G L E N V A S S I R H Y N A E L V
82410 CGGGGCTGTTGCAGACCCCCGGCTACGCCACCGCGCTCTTCGAGCACAACCGGCCCGAGCTGGGCGAGGAGGAGCGAAAGAAGGCGGTGGGC
      >P G L L Q T P G Y A T A L F E H N R P E L G E E E R K K A V G
82502 TTCCGGACTCAGCGGCAGGGGCTGCTGGCCCGGCGGCTGCCCCCGGCCCCCGAGCTGACCGTGATCCTCAGCGAGGCGGTGCTGCGCCGCCC
      > F R T Q R Q G L L A R R L P P A P E L T V I L S E A V L R R P
82594 GGTGCCGGGCCGATCGGTGATGGCCGACCAGCTCCGGCACCTGCTGGCCGTCGGCGAACGGCACAACATCACCGTACGGGTGCTGCCGCTGG
      > V P G R S V M A D Q L R H L L A V G E R H N I T V R V L P L
82686 CCGCCGGGCCGCCGCTGGCCGCCGAGGCCGGCACGTTCGTGCTGCTCGACTTCCCGCTCTCGGCGCTCGGCAGCCCGACCGAGCCGCCGACC
      >A A G P P L A A E A G T F V L L D F P L S A L G S P T E P P T
82778 GTCTACGTCGAGGGGCTCACCGGCGCGCTCTACCTCGACCAGCCGACGGAGATCGCCGCGTACGAACGGGTCTGGAGGGGTCTGGATTCGCT
      > V Y Y V E G L T G A L Y L D Q P T E I A A Y E R V W R G L D S L
82870 CGCCCTCGGCGCGCGACAATCAGCGGAGCTGATCGATGCCATCCGGGGAGAGTGCTATGAGTGATCTGACCGGCGCCCGCTGGCGCACCAG
      > A L G A R Q S A E L I D A I R G E C Y E •
82961 CACCCGCAGCGGCACCAACGGCGGGGACTGCGTCGAGGTGGCCGACAACCTCACCGGCATCGTCGGCGTCCGGGACAGCAAGGACCCGGGCG
83053 GGCCGGCCCTGACCGTCCCGCCCGCCGCCTGGTCCGCCTTCGTCACCGAGGTCAAGGCCAACCGCCTCACCCGCTGACAGCTCCGCAACGAA
83145 CCAACCCCCGGCTACGCCTCAGACGCGGCCAGCGCCCCAGGGCTGCCCACGCCTCAGACAGCCCGCGCCTCAGACGTGCCTGCGCCTCAGAC
83237 AGCCCGGGCCGCAGGGGCGCGTGCGCCTCAGACGGCCCGGGCCTCAGGCGCGCTTGCCGAGGGCGGCGTCGACCGCCTTGCCCAGGGCGGT
                                                    <• A R K G L A A D V A K G L A T
83328 GACGACCAGGGCCACCGAGGGGCGGACCACCGAGTCGTCCAGGCTGACGGTGCCGGAGAAGCCGGCCCCGCCCGCGATCTCCTCCAGCCGAC
      < V V L A V S P R V V S D D L S V T G S F G A G G A I E E L R R
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Figure 11V

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83420 GCCGGGCGTCGACGGCGGCGTCGCCGGTCAGGCCGAGCGCCGGCTCCATCCGGAGCACCGCGACCAGGGTGGCCAGCGCCGCCGTCGCCTCG
      <  R  A  D  V  A  A  D  G  T  L  G  L  A  P  E  M  R  L  V  A  V  L  T  A  L  A  A  T  A  E
83512 TCGGGGATCTGCCCGCCGGCCAGCGCCTCGGCCAGCCGCCGCCGGGAGTCCTCCTCCACGGTGGCGTCCGCCGTCGGGTAGCGGTGCACGTG
      <D  P  I  Q  G  G  A  L  A  E  A  L  R  R  R  S  D  E  E  V  T  A  D  A  T  P  Y  R  H  V  H
83604 GATGAAGCCCAGCTCGGTCTCCTCGACGTCGCGCACCACGCCCCGGGCGACCAGGTCGCCGAGGATCCGGTCGCGCAGGCCGTGGCGCAGCC
      <  I  F  G  L  E  T  E  E  V  D  R  V  V  G  R  A  V  L  D  G  L  I  R  D  R  L  G  H  R  L  R
83696 GCTGCACCCAGGAGGACGGGGTGTGCGGCGTGTCGGCGGCCATCCGGCCCAGGACCTCGTCCAGGATCGGTTCGCCGGTGGGCGCGGGGTCC
      <  Q  V  W  S  S  P  T  H  P  T  D  A  A  M  R  G  L  V  E  D  L  I  P  E  G  T  P  A  P  D
83788 GTGACCACCAGGTTCCCATCGACGTACGCGACCCGGCCGGCGAGGGCCAGCTCGATCAGGACGGCGGCGGCCATCCCGAGGTCGAGGCTGAT
      <T  V  V  L  N  G  D  V  Y  A  V  R  G  A  L  A  L  E  I  L  V  A  A  A  M  G  L  D  L  S  I
83880 CCGCGGCATGGTCGCCTTGCCGGATTCGTCGTCGTACGCGAGGAGCAGCAATTCCTCGGCCAGCGCAACACCAGTCATGGCCGGAGACGG
      <  R  P  M
83970 TAGCGCCTGAGCGCACCCCGTGCGCCCCCAACTCGCCCACGAGCGCACTCGCCCGGTGAGAGGGGAACCCCGCTATACCGCAGGCGTTAACA
84062 GGGGGCCCTTCCTTGCGATCAGAAGCGGGGCATACCGCCGAACTGGCGGTCGCCGGCGTCGCCGAGGCCCGGCACGATGAACATCCGGTCG
                        <  o  F  R  P  M  G  G  F  Q  R  D  G  A  D  G  L  G  P  V  I  F  M  R  D
84153 TTGAGGCTCTCGTCGATCGCGGCGGTGACGAGGCGCAGCGGCAGGCCGGACTGCTCCAGCCGGGCGATGCCGACGGGCGCGGCGAGCACGCA
      <N  L  S  E  D  I  A  A  T  V  L  R  L  P  L  G  S  Q  E  L  R  A  I  G  V  P  A  A  L  V  C
84245 GAGCACGGTGATGTCGGTGCAGCCCCGCTCGGCCAGCAGCCGGCAGCAGTGCTCCAGGGAGCCGCCGGTGGCCAGCATCGGGTCGAGGACCA
      <  L  V  T  I  D  T  C  G  R  E  A  L  L  R  C  C  H  E  L  S  G  G  T  A  L  M  P  D  L  V  L
84337 GCACGGGCAGGCCGGCGAGGTCGCGCGGCAGCGACTCCATGTACGCGCGCGGCTCGTACGTCTCCTCGTCGCGGGCGAGGCCGACGAAGCCC
      <  V  P  L  G  A  L  D  R  P  L  S  E  M  Y  A  R  P  E  Y  T  E  E  D  R  A  L  G  V  F  G
84429 ATGGACGACTCGGGGAGCAGGGCGAGCGCGGCGTCGGCCATGCCGAGACCGGCCCGCAGCACGGGTACCAGCAGCGGCGGGTTGGCCAGCCG
      <M  S  S  E  P  L  L  A  L  A  A  D  A  M  G  L  G  A  R  L  V  P  V  L  L  P  P  N  A  L  R
84521 GGTGCCCTCGGCGTCGGTGACGGGGGTCTGCACCGGGTACTTCTCGACGGGGAAGGAGCGGGCGGCCTCGTACACGAGCATGGTGGTGAGCT
      <  T  G  E  A  D  T  V  P  T  Q  V  P  Y  K  E  V  P  F  S  R  A  A  E  Y  V  L  M  T  T  L  E
84613 CGTGCAGCGCGGCCCGGAAGTTGGAGGAGTCGGTGCGCGCGTCCCGCATGGCGGTCAGCCGCGACTGGGCGAGCGGATGGTCAATGACGTGT
      <  H  L  A  A  R  F  N  S  S  D  T  R  A  D  R  M
84705 ACGTCCACGATCGCCCAACCTACCGAACGCCCGGGCCCCGAGACACGAGGAGCGACGCCGCTCACCCGGCCCGTGCGGCAACCCTGGACGGT
84797 TGGCGTTCGAAGGTAGGGCAGGTGCCCAAGGTCGGGCCCCGACCTCGCCGCGTGATCAAGATCACGAGGCGTGCGGGTGCGTAGACTTCCGGG
84889 CATGACGGCGACAGCGACGTCGGCCCGGTCGGACCTCTCCGAGCTGGGACGATCCGAGACCGCTTTGCGGAACTTCCTGCACGGCCTGCCG
       >  M  T  A  T  A  T  S  A  R  S  D  L  S  E  L  G  R  S  E  T  A  L  R  N  F  L  H  G  L  P
84980 GGCGTGGACCAGGTCGGCGCGGAGCAGCGGGCGGCCCAGCTCGGCACCCGCTCGATCAAGACCACGGCCAAGGCCCGGGCGATCGACCTGGC
      >  G  V  D  Q  V  G  A  E  Q  R  A  A  Q  L  G  T  R  S  I  K  T  T  A  K  A  R  A  I  D  L  A
85072 GATCCGGATGGTCGACCTGACCACCCTGGAGGGGGCCGACACCCCCGGCAAGGTGCGGGCGCTCGCGGCCAAAGCACTGCGCCCCGACCCGG
      >  I  R  M  V  D  L  T  T  L  E  G  A  D  T  P  G  K  V  R  A  L  A  A  K  A  L  R  P  D  P
85164 CCGACCCGTCCTGCCCGCACGTCGGCGCAGTCTGCGTCTACCCGGCGATGGTCCCGTACGTGGCCGAGGTGCTGCGCGGATCCGCCGGGTCC
      >A  D  P  S  C  P  H  V  G  A  V  C  V  Y  P  A  M  V  P  Y  V  A  E  V  L  R  G  S  A  G  S
85256 GGGCGGCCGTCCGGCGGACCGGACGGCAACGCGCCGGCCGGACCCGGCGTGGTGCACCTGGCCAGCGTGGCCACCGCGTTTCCGTCCGGGCA
      >  G  R  P  S  G  G  P  D  G  N  A  P  A  G  P  G  V  V  H  L  A  S  V  A  T  A  F  P  S  G  Q
85348 GGCACCCCTGGAGGTCAAGCTCGCCGACACCCGGGCCGCAGTGGCGGCTGGCGCGGACGAGATCGACATGGTGATCAACCGGGGCGCGTTCC
      >  A  P  L  E  V  K  L  A  D  T  R  A  A  V  A  A  G  A  D  E  I  D  M  V  I  N  R  G  A  F
85440 TGGCCGGCCGCTACCGCGAGGTCTACGACGAGATCGTGGCCACCAAACAGGCGTGCGGGGACGCCCACCTCAAGGTGATCCTGGAAACCGGC
      >L  A  G  R  Y  R  E  V  Y  D  E  I  V  A  T  K  Q  A  C  G  D  A  H  L  K  V  I  L  E  T  G
85532 GAGCTGGCCACGTACGACAACGTGCGCCGGGCGTCCTGGCTGGCCATGCTGGCCGGCGGCGACTTCATCAAGACCTCGACGGGCAAGGTTCC
      >  E  L  A  T  Y  D  N  V  R  R  A  S  W  L  A  M  L  A  G  G  D  F  I  K  T  S  T  G  K  V  P
85624 CGTCGCGGCGACCCTCCCGGTGACGCTGGTGATGCTGGAGGCGGTCCGCGACTTCCGCGCCGCCACCGGGCGGCAGGTCGGCGTGAAGCCGG
      >  V  A  A  T  L  P  V  T  L  V  M  L  E  A  V  R  D  F  R  A  A  T  G  R  Q  V  G  V  K  P
85716 CCGGCGGCATCAAGAACACCAAGGACGCGATCAAGTACCTGGTTATGGTCAACGAGACCGTCGGCCCGGACTGGCTGGACCCGGACTGGTTC
      >A  G  G  I  K  N  T  K  D  A  I  K  Y  L  V  M  V  N  E  T  V  G  P  D  W  L  D  P  D  W  F
85808 CGGTTCGGCGCGTCCAGCCTGCTCAACGACCTGCTCATGCAGCGCACCAAGCTGACGACCGGCGTCTACTCCGGTCCCGACTACTTCACCCT
      >  R  F  G  A  S  S  L  L  N  D  L  L  M  Q  R  T  K  L  T  T  G  V  Y  S  G  P  D  Y  F  T  L
85900 GGACTGAGCGTGATCTTCGAATACGCGCCCGCCCCCGAGTCCCGCTCGGTGGTGGACCTCAAGCCCTCGTACGGGCTGTTCGTCGACGG
      >  D  •  >  V  I  F  E  Y  A  P  A  P  E  S  R  S  V  V  D  L  K  P  S  Y  G  L  F  V  D  G
85989 GGAGTTCGTCGACCCGGCCGACGGCGGCGGCTTCAAGTCGGTCAACCCCGCCTCCGAGGAGGTGCTCGCCGAGATCGCCGAGGCGGGCAGCG
      >  E  F  V  D  P  A  D  G  G  F  K  S  V  N  P  A  S  E  E  V  L  A  E  I  A  E  A  G  S
86081 CCGACGTGGACCGGGCGGTCCGCGCCGCCCGGACGGCGTACGAGAAGGTGTGGGGCCCGATGCCGGGCCGGGACCGGGCCAAGTACCTGTTC
      >A  D  V  D  R  A  V  R  A  A  R  T  A  Y  E  K  V  W  G  P  M  P  G  R  D  R  A  K  Y  L  F
86173 CGGATCGCCCGGATCATCCAGGAGCGCTCCCGCGAGCTGGCCGTGCTGGAGTCCCTGGACAACGGCAAACCGATCCGGGAGTCCCGGGACGT
      >  R  I  A  R  I  I  Q  E  R  S  R  E  L  A  V  L  E  S  L  D  N  G  K  P  I  R  E  S  R  D  V
86265 CGACCTGCCGCTGGTCGCCGCGCACTTCTTCTACTACGCGGGCTGGGCAGACAAGCTGCCGTACGCGGGCTTCGGCCCGAACCCCCGGCCGC
      >  D  L  P  L  V  A  A  H  F  F  Y  Y  A  G  W  A  D  K  L  P  Y  A  G  F  G  P  N  P  R  P
86357 TCGGCGTGGCCGCGCAGGTCATCCCGTGGAACTTCCCGCTGCTCATGCTCGCCTGGAAGATCGCCCCGGCGCTGGCCGCCGGCAACACGGTG
      >L  G  V  A  A  Q  V  I  P  W  N  F  P  L  L  M  L  A  W  K  I  A  P  A  L  A  A  G  N  T  V
86449 GTGCTCAAGCCGGCGGAGACCACCCCGCTGACCGCGCTGCTGTTCGCCGAGATCTGCCAGCAGGCCGAGCTGCCGGCCGGCGTGGTCAACAT
      >  V  L  K  P  A  E  T  T  P  L  T  A  L  L  F  A  E  I  C  Q  Q  A  E  L  P  A  G  V  V  N  I
86541 CGTCACCGGCGCGGGCGACACCGGCCGGGCGCTGGTCGAGCACCCGGGCGTGGACAAGGTCGCGTTCACCGGCTCGACCGAGGTCGGCAAGG
      >  V  T  G  A  G  D  T  G  R  A  L  V  E  H  P  G  V  D  K  V  A  F  T  G  S  T  E  V  G  K
86633 CCATCGCCCGGTCCGTCGCGGGCACCGGCAAGAAGGTCACCCTGGAGCTGGGCGGCAAGGCCGCGAACATCGTCTTCGACGACGCCCCGGTC
      >A  I  A  R  S  V  A  G  T  G  K  K  V  T  L  E  L  G  G  K  A  A  N  I  V  F  D  D  A  P  V
86725 GACCAGGCGGTCGAGGGGATCGTCAACGGCATCTTCTTCAACCAGGGGCACGTCTGCTGCGCCGGGTCGCGGCTGCTGGTCCAGGAGTCGGT
      >  D  Q  A  V  E  G  I  V  N  G  I  F  F  N  Q  G  H  V  C  C  A  G  S  R  L  L  V  Q  E  S  V
86817 CGCCGAGCAGGTGCTGGAGTCGCTGAAGCGCCGAATGGCGCTGCTGCGGGTCGGCGACCCGTTGGACAAGAACACCGACATCGGGGCGATCA
      >  A  E  Q  V  L  E  S  L  K  R  R  M  A  L  L  R  V  G  D  P  L  D  K  N  T  D  I  G  A  I
86909 ACTCGGCCGCCCAGCTCGCCCGCATCCGCGAGCTGTCCGCCGCGGGCGAGGCCGAGGGGGCGGAGCGCTGGTCGCCGCCGTGCGAGCTGCCC
      >N  S  A  A  Q  L  A  R  I  R  E  L  S  A  A  G  E  A  E  G  A  E  R  W  S  P  P  C  E  L  P
87001 GAGCGCGGGTTCTGGTTCGCGCCGACGATCTTCACGGGGGTCACCCAGGCGCACCGGATCGCCCGGGAGGAGATCTTCGGTCCGGTGCTGTC
      >  E  R  G  F  W  F  A  P  T  I  F  T  G  V  T  Q  A  H  R  I  A  R  E  E  I  F  G  P  V  L  S
87093 CGTGCTGACCTTCCGCACCCCGGCCGAGGCCGTCGAGAAGGCCAACAACACGCCGTACGGGCTGTCGGCCGGGATCTGGACCGACAAGGGCT
      >  V  L  T  F  R  T  P  A  E  A  V  E  K  A  N  N  T  P  Y  G  L  S  A  G  I  W  T  D  K  G
```

Figure 11W

```
87188 CCCGGATCCTGTGGATGGCCGACCGGCTGCGCGCCGGGGTGGTGTGGGCCAACACGTTCAACAAGTTCGACCCGACCTCGCCGTTCGGCGGG
      >S  R  I  L  W  M  A  D  R  L  R  A  G  V  V  W  A  N  T  F  N  K  F  D  P  T  S  P  F  G  G
87277 TACAAGGAGTCGGGCTACGGTCGCGAGGGCGGCCGGCACGGGCTGGAGGGGTACCTCGGTGTCTGAGCGGGTCGCGGTACGCAAGACGTAC
      >Y  K  E  S  G  Y  G  R  E  G  G  R  H  G  L  E  G  Y  L  G  V  •
87366 AAGCTCTTCATCGGCGGGAAGTTCCCGCGCAGCGAGTCGGGACGGTCGTATCTCGTGCAATCCGCGAACGTGTCGCTGGCCTCCCGCAAG
                                                                      >V  Q  S  A  N  V  S  L  A  S  R  K
87458 GACGCGCGGGACGCCGTGGTCGCCGCCCGCGCCGCCGTGAAGGGCTGGGCCGGGGCGACCGCGTACAACCGGGGTCAGATCCTCTACCGGGT
      >D  A  R  D  A  V  V  A  A  R  A  A  V  K  G  W  A  G  A  T  A  Y  N  R  G  Q  I  L  Y  R  V
87550 CGCCGAGATGCTGGAGGGCCGCCGCGAGCAGTTCGTCGCGCTCGGCGTGCCGGCCGACGAGGTCGACGCGGCGATCGACCGCTGGGTCTGGT
      >A  E  M  L  E  G  R  R  E  Q  F  V  A  L  G  V  P  A  D  E  V  D  A  A  I  D  R  W  V  W
87642 ACGCGGGCTGGTCCGACAAGCTCCCCCAGGTGTACGGCGGTGCGAACCCTGTCGCCGGGCCGTACTTCAACCTGTCCGCGCCCGAGCCGACG
      >Y  A  G  W  S  D  K  L  P  Q  V  Y  G  G  A  N  P  V  A  G  P  Y  F  N  L  S  A  P  E  P  T
87734 GGGGTGGTGGCCGTGGTGGCCCCCGAGGCCCCCGCGCTGCTCGGCCTGGTCAGCGTGATCGCCCCGGCGATCGTCACCGGCAACACGGTGGT
      >G  V  V  A  V  V  A  P  E  A  P  A  L  L  G  L  V  S  V  I  A  P  A  I  V  T  G  N  T  V  V
87826 GGTGGCGGCCTCGCCGACCCAGCCCCTGGCCTCGGTGACCCTGGCCGAGGTGCTGGCCACCTCCGACCTGCCCGGCGGGGTGGTCAACGTCC
      >V  A  A  S  P  T  Q  P  L  A  S  V  T  L  A  E  V  L  A  T  S  D  L  P  G  G  V  V  N  V
87918 TGACCGGTGCGATCACCGAGACGGTGCCGACGCTCGCGGCGCACCTGGACGTCAACGCGATCGACCTGACCGGGGTGGGCGACGCGTCGCTC
      >L  T  G  A  I  T  E  T  V  P  T  L  A  A  H  L  D  V  N  A  I  D  L  T  G  V  G  D  A  S  L
88010 GCCACCGAGCTGGAGGTCAGGGCGGCGGAGAACCTCAAGCGGGTGATTCGGCCGGCCCCGGCCGACCACGACTGGTACGCCGACCCGGGCCT
      >A  T  E  L  E  V  R  A  A  E  N  L  K  R  V  I  R  P  A  P  A  D  H  D  W  Y  A  D  P  G  L
88102 CACCCGGATGACGACGCTGCTGGAGACGAAGACGGTCTGGCACCCCAAGGGCGTCTGAGCCCACCGACCCGTCCACCGACCCGCCCGCCAC
      >T  R  M  T  T  L  L  E  T  K  T  V  W  H  P  K  G  V  •
88193 CCGGCCGCCGGAGGCAGGGGTGGGCGGCGGGTGGGGTGGATCTACTACGAGGGGTAGGATTGCCGCGTGACTCGGTTGGGTGATCTTGAGC
88284 GGGCGGTGATGGACGTGCTGTGGGACACCGTCCCGGGCACGTCGGACGGGGTGACGGTGCGCGAGGTCGCCGAGGCCCTCGACGGCCGCGA
            >M  D  V  L  W  D  T  V  P  G  T  S  D  G  V  T  V  R  E  V  A  E  A  L  D  G  R  E
88375 GCTGGCGTACACGACGGTGATGACCGTGCTGGACCGGCTCGCCGGCAAGGGCATGGTGCGGCGCCAGCGGGAGGGGCGGGCCTGGCGCTACC
      >L  A  Y  T  T  V  M  T  V  L  D  R  L  A  G  K  G  M  V  R  R  Q  R  E  G  R  A  W  R  Y
88467 AGGCCGCGGCCAGCCGCGAGGCGCACATCGCCCAGCTCATGCTCGACGCGCTGGACCTCGGCGGCAGCCGGGACGCCGCGCTGGTGCGCTTC
      >Q  A  A  A  S  R  E  A  H  I  A  Q  L  M  L  D  A  L  D  L  G  G  S  R  D  A  A  L  V  R  F
88559 GCCCGGTCGGTGACCGGCACCGAGGCCGAGGTGCTGCGCGCCGCCCTCGGCGCCGAGGCGGGCGGCCCGCTGACCGACCGCGTCGACGCGCC
      >A  R  S  V  T  G  T  E  A  E  V  L  R  A  A  L  G  A  E  A  G  G  P  L  T  D  R  V  D  A  P
88651 GCGCGCCGACCGGGCCGGGCAGCCGGCCCTGGCCGACGAGGCGACGGACCGGTAGGGCCGCCGTCATGGCGTACGCCGTGCACTTCGCCG
      >R  A  D  R  A  G  Q  P  A  L  A  D  E  A  T  D  R  •                >M  A  Y  A  V  H  F  A
88741 CGACGGTCCTGGCCTGCTACCTGACCGCTCAGGTCCTGGCGGCGTCCACCTGGACGTGGCGGGCCCCCCGGATCGCGATCGTCTGCTGGCAG
      >A  T  V  L  A  C  Y  L  T  A  Q  V  L  A  A  S  T  W  T  W  R  A  P  R  I  A  I  V  C  W  Q
88833 GCGGTCGGGCTCGCGCTCGGGCTCTCCGCGATGGGCCTGCCGATGGCGCTCGGCGTGGCCGCGTACGACCGGCCGACCGGCAGCGCGTTGCT
      >A  V  G  L  A  L  G  L  S  A  M  G  L  P  M  A  L  G  V  A  A  Y  D  R  P  T  G  S  A  L  L
88925 CGCCCTGGCCACCGACCTGACCCACGGCACCCTGCCGGCCGGCCGGGCTCGGCGCGGTCCACCTCGGTCTGGTCGGGGTCGGGTTCGGCATCGGGG
      >A  L  A  T  D  L  T  H  G  T  L  P  A  G  L  G  A  V  H  L  G  L  V  G  V  G  F  G  I  G
89017 CGGCGCTGCTCGCCACGACGGTACGCAGCGTGCAGGCGACCGTCCGGGCCCAGCGGCAGCACCGGGACCTGCTCGCCCTGGTGGCCCGGCGG
      >A  A  L  L  A  T  T  V  R  S  V  Q  A  T  V  R  A  Q  R  Q  H  R  D  L  L  A  L  V  A  R  R
89109 GACCCGGAGGTGCCGGGGGCGCTGGTGCTGGACCATCCGAGCGCGGCGGCGTACTGCCTGCCGGGCGTGCGGCCCCGGGTGGTGGTCAGCGC
      >D  P  E  V  P  G  A  L  V  L  D  H  P  S  A  A  A  Y  C  L  P  G  V  R  P  R  V  V  V  S  A
89201 CGGGGCGCTCAGCATGCTCGACCGGGCCGAGCTGGCGGCGGTGCTGACCCACGAGCGGGCGCACGCCCAGGAGCGCCACGACCTTGTGCTGC
      >G  A  L  S  M  L  D  R  A  E  L  A  A  V  L  T  H  E  R  A  H  A  Q  E  R  H  D  L  V  L
89293 TGCCGTTCACCGCGCTGTGCCGTGCGCTGCCCTGGTTCCGTTGGGTACGCGACGCGCACGAGCGGGTCGCCCTGCTGGTCGAGATGCGCGCC
      >L  P  F  T  A  L  C  R  A  L  P  W  F  R  W  V  R  D  A  H  E  R  V  A  L  L  V  E  M  R  A
89385 GACGACAAGGCCCGGGAGCTGCACGCCGAGGCTCCCCTCGCGGGGGCGTTGCGCCGGTTCGCCGCGGCCGGCCACCGGATCGCGCCGGCCGG
      >D  D  K  A  R  E  L  H  A  E  A  P  L  A  G  A  L  R  R  F  A  A  A  G  H  R  I  A  P  A  G
89477 CACCCTCGGCCTGGGCGACCGGGACCTGGACGTCCGGGTCCAGCGGCTGCTGGTCGCCGACCGGCCGCCCCGGCTGATCGGGGCCGCCGCGC
      >T  L  G  L  G  D  R  D  L  D  V  R  V  Q  R  L  L  V  A  D  R  P  P  R  L  I  G  A  A  A
89569 TGGCGGTGGCGGTCACCCTGGTCGCGCTGCCGGTCTCCCTCTTCCTGAGCTGACGCCCGACCCGGACACGTCCGACCCGGACACGCGCGAC
      >L  A  V  A  V  T  L  V  A  L  P  V  S  L  F  L  S  •
89660 CGGACACGTCCGACCCGGACGCCTCGCCCGAGTTGGGCCCGTGTCCCACGGGGCCGGCTCGCCTGCCCGTTGCCGGGCCACCGACATGCGGG
89752 GCGATAGGTAGAGAGCCTACGTGTAGTCTTCCTACGACAAGGGAGCCTACTACCGGAGGGCGGCCATGGATCAACTGCTCCTCGCCCGTC
                                                                        >M  D  Q  L  L  A  R
89842 TCCAGTTCGCCACGACCACCTCGCTGCACTTCCTCTTCGTCGTCGTCACGCTCGGTCTGGTCACCCTGCTCGTCGGGCTCCAGACGGCCTGG
      >L  Q  F  A  T  T  T  S  L  H  F  L  F  V  V  V  T  L  G  L  V  T  L  L  V  G  L  Q  T  A  W
89934 ACGATCACCGGCAATCCCGTCCACGAGCGGCTGACCCGGTTCTGGGGTCAGCTCTACGTGATCAACTACGTGCTCGGCATCGCCACCGGCCT
      >T  I  T  G  N  P  V  H  E  R  L  T  R  F  W  G  Q  L  Y  V  I  N  Y  V  L  G  I  A  T  G  L
90026 GCTCATGGAGTTCCAGTTCGGGCTGAACTGGAGCGGCCTGTCGCGCTACGTCGGCAACGTCTTCGGCGCCCCGCTGGCGATCGAGACCCTGG
      >L  M  E  F  Q  F  G  L  N  W  S  G  L  S  R  Y  V  G  N  V  F  G  A  P  L  A  I  E  T  L
90118 TCGCGTTCTTCCTGGAGTCCACGTTCCTCGGGATGTGGATCTTCGGCTGGCACCGGCTGCGCCGGGGCGTGCACCTCGCGCTGCTGTGGGGC
      >V  A  F  F  L  E  S  T  F  L  G  M  W  I  F  G  W  H  R  L  R  R  G  V  H  L  A  L  L  W  G
90210 GTGGCGCTGACCGCGTACGCCTCGGCGTTCTGGGTCATGGTGGCGAACGCCTGGCTGCAGAACCCGGTCGGCTACGAGGTGCGCGACGGGGT
      >V  A  L  T  A  Y  A  S  A  F  W  V  M  V  A  N  A  W  L  Q  N  P  V  G  Y  E  V  R  D  G  V
90302 GGCCCACCTGACCGACTTCGGCGCGTTGCTGACCAATCCCACCTTCGGCCTGGCCTTCGGGCACGTGGTCGCCGCCGCCCTGCTCACCGGCG
      >A  H  L  T  D  F  G  A  L  L  T  N  P  T  F  G  L  A  F  G  H  V  V  A  A  A  L  L  T  G
90394 GGATGCTGATGGCGGCGGTGAGCGCCTGGCACCTGATCCGGCGCACCCCGGACCACGCGCTGTTCCGCACGTCGCTGCGGATCGGCCTGGTC
      >G  M  L  M  A  A  V  S  A  W  H  L  I  R  R  T  P  D  H  A  L  F  R  T  S  L  R  I  G  L  V
90486 ACCGCGGCGGTCTCGATCAGCCTGGTGCAGGGCTTCGGCTTCGCCCAGTTCGGGCCGGTCGGGCAGACGCAGCCCACCAAGTTCGGCGGCGG
      >T  A  A  V  S  I  S  L  V  Q  G  F  G  F  A  Q  F  G  P  V  G  Q  T  Q  P  T  K  F  G  G  G
90578 CGCGCAGCGCGACGCCCTGGTCGCCGAATGGACCTCCCGGTTCGGGCCCGGCGACTACACCCCGCCCGTGCTGGCCGACGTCGGGCTCGGTT
      >A  Q  R  D  A  L  V  A  E  W  T  S  R  F  G  P  G  D  Y  T  P  P  V  L  A  D  V  G  L  G
90670 TCATGATCCTGATCGGCCTCCTCCTGGGCTGTCTGTGGCTGCTGCTCCCCCTGCTCTGGCGGGACTGGTTCATCCGGCTGCGCTTCCCGCTC
      >F  M  I  L  I  G  L  L  L  G  C  L  W  L  L  L  P  L  L  W  R  D  W  F  I  R  L  R  F  P  L
90762 TGGCTGATCCTGCTGGCGCTGCCGCTGCCCTTCGTCGCGGTGATCCTCGGCTGGATCGCCCGTGAGGTGGGCCGCCAGCCCTGGGTCGCGTA
      >W  L  I  L  L  A  L  P  L  P  F  V  A  V  I  L  G  W  I  A  R  E  V  G  R  Q  P  W  V  A  Y
```

Figure 11X

```
90854 CGGGCTGCTTTCCACCGAGCGGGCGGTCTCGCCGGTCGCGCCCGGGGTGATGCTCGCCTCGCTGATCGGCTTCACCCTGCTGCTCGGCGGGC
      > G L L S T E R A V S P V A P G V M L A S L I G F T L L L G G
90946 TCGCCGTCGCCAACTGGGTGCTGTTCGCCCGGTACGCCGCCCGGGGAGCCGCCGATCCCGCCCTAGGCCGCCGGCCCGGCCCAGCCGCCGAC
      >L A V A N W V L F A R Y A A R G A A D P A L G R R P G P A A D
91038 GAGTCCCGTCCCGTCCCCGTCCTCGGCTGAGGAGGCCCCTGTGGAACTCGCCTGGTACGCCCTGCTCGGGCTCTTCCTCGCCGGCTACC
      > E S R P V P V L G ∘          > V E L A W Y A L L G L F L A G Y
91127 TGGTCCTCGGCGGCTACGACTACGGCGTCGGCCTGCTGCTCGCCCGGGGCGGCCCGCCGGCCCGCCGCCGGGCGGCCCTCACCGCCGTGGGC
      >L V L G G Y D Y G V G L L L A R G G P P A R R R A A L T A V G
91219 CCGTTCTTCCTCGGCAACGAGGTCTGGCTGGTGGCGACCGTCGGCATTCTGTTCGGCGCGTTCCCCACCCTGGAGGGGGAACTGCTGTCCGG
      > P F F L G N E V W L V A T V G I L F G A F P T L E G E L L S G
91311 CTTCTACCCCGTCGTCGCCGCCGCGCTGGCCGGGGTGATCATGGTGACCGTCGGCGTGCAACTGCGCAGCCGCCCGACCGACGAGCCGACCC
      > F Y P V V A A A L A G V I M V T V G V Q L R S R P T D E P T
91403 GCGCCGCCTGGGACCGGATGGTGGCCGCCGGGAGCCTGCTCGCCGCGTTCGGCTGGGGGGCGCTGCTCGCCGGGCTGCTCCAGGGCGTACCG
      >R A A W D R M V A A G S L L A A F G W G A L L A G L L Q G V P
91495 CTGGCCGCCGACGGGCACGTCACGGGCGTCGGCCACGTGGCCACCCCGTTCGCGGCCCTCGCCGGGCTGGCGATGACGGCCCTGGTGGCGGT
      > L A A D G H V T G V G H V A T P F A A L A G L A M T A L V A V
91587 GCACGGTGCGACGTTCCTCACGCTCCGGCTGTCGGCCGCCGACGCCGCACCGCTGGCCCGTACCGCCCGCCGGCTGGTCGCGGTGGCGCTCG
      > H G A T F L T L R L S A A D A A P L A R T A R R L V A V A L
91679 CCGCCGTCGCCCTGGCCGCCGTCGCGGGCGCGCTCTCCGATCGGGTACGCGCCGCGACGCAGCGCCCGCTGCCGGCCGTACTGCTGCCGTTG
      >A A V A L A A V A G A L S D R V R A A T Q R P L P A V L L P L
91771 GTACTGGTGGCGGCGCTGCTGGTGGCCCGGGCGGCGCACGCGCGGCACCTGCCCGGGGTGGCCTTCGCCGCCACTTCGGCGGCGCTGGCGCT
      > V L V A A L L V A R A A H A R H L P G V A F A A T S A A L A L
91863 GCCGGTGGCGGGAGTCGGCGCGGCGTTGTGGCCCTACGCGCTGGTCTCCACCGTCGCACCGACGGCATCACTGAGCGTGACCGACGCGGCGG
      > P V A G V G A A L W P Y A L V S T V A P T A S L S V T D A A
91955 CCAGCGGGCCGACGCTGACGGTGCTGGGCTGGCTGGCGCTACCGCTCCTGCCGGCCCTACTAGGCTTCCAGGCGATGTGCTGGTGGGTGTTC
      >A S G P T L T V L G W L A L P L L P A L L G F Q A M C W W V F
92047 CGGGGACGAACCGACGGCAGGGCACCGGTGTACTGGTGAGCCGCCGTCCCTTCGACCCACGTCTGCTCCGCCGGGTCCCCGCGGCCCGGCG
      > R G R T D G R A P V Y W ∘
92138 CGACCTCGCCGTGCTCGCGGTGCTCGGCGGGCTGACGGCGCTGCTGGTCGTGGGGCAGGCCACCGCGCTGGCCACGGTGCTGGCCGCCGCG
                > V L A V L G G L T A L L V V G Q A T A L A T V L A A A
92229 CTCGACGGGCGGTTGGCCCGGCCGGCGCTCGCCGGTTTCCTGGCCGCCGTGGTGGGGCGGGCGCTGGTCGCCTGGGCCCAGGGCACGGTGGC
      > L D G R L A R P A L A G F L A A V V G R A L V A W A Q G T V A
92321 GGCGCGGGCCGCCGCGACGGTCAAGGCGGCGCTGCGGGCCGACCTGCTCGCCGCCGTCGGCCGGCACGGTCCCGGCTGGGTCGCCGGGCAGC
      > A R A A A T V K A A L R A D L L A A V G R H G P G W V A G Q
92413 GGGCCGGGCAGCTCGCCACCCTGGCCGGGCGGGGGCTGGACGCCCTGGACGCCTACTTCACCGGGTACCTTCCGCAGCTCGTGCTCAGCGTC
      >R A G Q L A T L A G R G L D A L D A Y F T G Y L P Q L V L S V
92505 ACCGTCCCGGTGGCCGTGCTGGCCCGGATCACCTTCGCCGACTGGGGCTCGGCCGTCATCGTCGCGCTGACCCTGCCGCTGATCCCGGTCTT
      > T V P V A V L A R I T F A D W G S A V I V A L T L P L I P V F
92597 CGGGGCGCTGCTCGGCTGGCAGGCGCAGGCCGCCACCGAGCGGCAGTGGCGGCGGCTGTCGACGCTCGGCGGGCACTTCCTCGACATGGTCG
      > G A L L G W Q A Q A A T E R Q W R R L S T L G G H F L D M V
92689 CCGGCCTGCCCACGCTGCGCGCGTTCGGCCGGGCCCGGGGCCAGGTCGAGGTGGTCCGCCGGATGGCCGACGGGCACCGCGCCGCGACGATG
      >A G L P T L R A F G R A R G Q V E V V R R M A D G H R A A T M
92781 CGCACGCTGCGGATCGCGTTCCTGTCCGCGCTGGTGCTGGAGCTGGTCGCCACCCTGTCGGTGGCGCTGGTCGCGGTGCCGGTGGGCATCCG
      > R T L R I A F L S A L V L E L V A T L S V A L V A V P V G I R
92873 GCTGCTCGGCGGCGGGCTGGCGCTGTCCACCGCGCTGCTGGTGCTGCTGCTCACCCCGGAGGCGTACCTGCCGCTGCGGGCGGCCGGCAGCC
      > L L G G G L A L S T A L L V L L L T P E A Y L P L R A A G S
92965 GGTTCCACGCCAGCATGGAGGGGCTGGCCGCGCTGGACGAGGCACTGACCCTCTCCGCCGCCGACCCGACCGCCACGGCCACCGCCGGGGTCG
      >R F H A S M E G L A A L D E A L T L S A A D P T A T A T A G S
93057 CGGCCCGTCCCCGACGGGCGCGCCGAGATCCGGTTCGAGGGCGTGACCGTCGCGTACGAGCGGACCGTGGCGCTACGGGACGTCACGCTGAC
      > R P V P D G R A E I R F E G V T V A Y E R T V A L R D V T L T
93149 AATCCGGCCCGGCGAGCGGATCGCGATCGTCGGGCCGAGCGGCGCGGGCAAGAGCACCCTGCTCAACCTGCTGCTCGGCTTCGTCGCCCCGA
      > I R P G E R I A I V G P S G A G K S T L L N L L L G F V A P
93241 CGCAGGGCCGGGTCACCGTGGGTGGCGTCGACCTGGCCGGCGCGGACCCGGACGGCTGGCGGCGTCAGGTCGCCTGGGTGCCGCAACGGGCC
      >T Q G R V T V G G V D L A G A D P D G W R R Q V A W V P Q R A
93333 CACCTCTTCGCCGCCTCGCTGACCGACAACATCCGGCTCGGTGCCCCCGGCACGCCCGACGCCGCGCTCGCCGGCGCGGTCGCCGCCGCCGC
      > H L F A A S L T D N I R L G A P G T P D A A L A G A V A A A A
93425 GCTGGACGAGGTGGTCGCCGCCCTGCCCGACGGGCTCGACACCGTGCTCGGTGAGCGCGGGCACGGCCTGTCCAGCGGCCAGCGGCAGCGGG
      > L D E V V A A L P D G L D T V L G E R G H G L S S G Q R Q R
93517 TCGCCCTGGCCCGGGCGTTCCTGCGGGACGCGCCGGTGGTGCTGCTGGACGAGCCGACCGCGCGGCTGGACACCGCCAGCGAGGCCGGGGTG
      >V A L A R A F L R D A P V V L L D E P T A R L D T A S E A G V
93609 CTGGCCGCCACCCGCCGGCTCGTCGCCGGGCGAACCGCCCTGTTGGTGGCCCACCGGCCGGCGCTGCTCTCCGACGCCGACCGGATCCTGCG
      > L A A T R R L V A G R T A L L V A H R P A L L S D A D R I L R
93701 GGTCGAGGAAGGCCGGGTCACCGAGCTGACCACCACCCCGGCCACAGGGGTGACCCCCGGCCCCGGCGAGGCGGCTGCCGGACCGGCCGGGC
      > V E E G R V T E L T T T P A T G V T P G P G E A A A G P A G
93793 AGGTCGCCCCCGCCCCGGCCGGAGAGGGGGCGGCCCGATGAGCACCGGTCCCGCCGACGACGCCTTCGCCATCCCGCTGCCGGCCGACGGG
      >Q V A P A P A G E G A A R ∘
                                  > M S T G P A D D A F A I P L P A D G
93884 GCCCCGGTGGCCGGCGGCAGCGTCCGGGCCGCCGAGCGGGCCGTGCTCCGGCTGGCCCGGCCGTACCTGGGCCGGCTGGTCGGCGCGGGTCT
      > A P V A G G S V R A A E R A V L R L A R P Y L G R L V G A G L
93976 GCTCGCCGCCGCCACCGAGTTCGCCGGGCTGGCCCTGATGGCCACCGCCACCTGGCTGCTGATGAGCGCCGCCGGTCGGCCACCACTGGACC
      > L A A A T E F A G L A L M A T A T W L L M S A A G R P P L D
94068 GGCTCACCGTGGCGATCGTCGCGGTCCGGGCGCTGGCGATCAGCCGAGGCGTGTTCCGCTACACCGAGCGCCTCGCCGGCCACGATGCCGTG
      >R L T V A I V A V R A L A I S R G V F R Y T E R L A G H D A V
94160 CTGCGGATGATCACCGACGTCCGGGCCGGGGTCTTCGCCGCCCTGGCCGCCCGGCGCGACGCCGCCCGGCAGCGCACCGGGGACGCGCTGAG
      > L R M I T D V R A G V F A A L A A R R D A A R Q R T G D A L S
94252 CCGGCTCGTGTCCGACGTGGAGGCCGTGCAGGACCTGCTGCTGCGGGTGCTCGTCCCGGGGGCCGCCGCCACGGTGGTCAGCGTGCTGGCCG
      > R L V S D V E A V Q D L L L R V L V P G A A A T V V S V L A
94344 TGGCCGGGGCCACCACCATCTCGCTCCCCGCCGCCGGGGTGCTGGCGCTGGGCCTGCTCGTCGCCGGGGTGGCCCTGCCGCTCGCGGCCACC
      >V A G A T T I S L P A A G V L A L G L L V A G V A L P L A A T
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Figure 11Y

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94436 GCGCTGACCCGGCACGCCGCCGACCGGGTGGCCCCGCTGCGCGGCGCGCTCGCCACGGACGCCGTGGACCTTGTCCACGGCGCCGCCGACCT
      > A  L  T  R  H  A  A  D  R  V  A  P  L  R  G  A  L  A  T  D  A  V  D  L  V  H  G  A  A  D  L
94528 GGCCGCGTTCGGTGCCACCGGGTACGCGCTGGACGCCGCCGCCGATCGGGCCCGCCGGCTGGCCCGGCTGGAACGACGGCTCGCCGCCACCG
      > A  A  F  G  A  T  G  Y  A  L  D  A  A  A  D  R  A  R  R  L  A  R  L  E  R  R  L  A  A  T
94620 GCTTCGCCGTGGACGCCGCCGGGGCGCTCGTCGCCGGGGTGACCGCCGGCACGGTGGTGGTCACCGCGCTGCGCGACGGCGTCGGCGGGGTG
      >G  F  A  V  D  A  A  G  A  L  V  A  G  V  T  A  G  T  V  V  V  T  A  L  R  D  G  V  G  G  V
94712 CTGGTCGGGGTGCTGGCGGTCGGTTCCCTGGCCGCCGTCGAGGTGGCGCTGGCGCTGGTCGGGGCCGCCCGGCAGCGCACCCAGCTCCGGGC
      > L  V  G  V  L  A  V  G  S  L  A  A  V  E  V  A  L  A  L  V  G  A  A  R  Q  R  T  Q  L  R  A
94804 CGGGCTGGTCCGGGTGGCCGCCCTGCTGACCGCCCCGCAGGCCGACGCGCCCGCCGCCACCCCGCCCGGTGCCGCCCGTGCCGCCGCCGTCG
      > G  L  V  R  V  A  A  L  L  T  A  P  Q  A  D  A  P  A  A  T  P  P  G  A  A  R  A  A  A  V
94896 GTGCCGGCCCGCACGACGTGCGCTTCGACGCGGTCACCGTGCGGTACCGGGCCGGCACCGCCCCGGCCCTGGACCGGGTCACCCTGGACCTG
      >G  A  G  P  H  D  V  R  F  D  A  V  T  V  R  Y  R  A  G  T  A  P  A  L  D  R  V  T  L  D  L
94988 CCGGCCGGCCGCCGGGTCGCCGTGGTCGGGCCGAGCGGCGCCGGCAAGAGCACCCTCGCCGCCGTCCTCACCGGCACGGTGCGACCCGAGCA
      > P  A  G  R  R  V  A  V  V  G  P  S  G  A  G  K  S  T  L  A  A  V  L  T  G  T  V  R  P  E  Q
95080 GGGCCGGGTCACCCTCGACGGGGCCGACCTGTCGGCGTACCCGGTCGAGGAACTGCCCCGGGCCGTCGGCGGCCTGCTCGCCGAGGCGTACG
      > G  R  V  T  L  D  G  A  D  L  S  A  Y  P  V  E  E  L  P  R  A  V  G  G  L  L  A  E  A  Y
95172 TCTTCCACGCCACGGTCCGGGAGAACCTGCTGCTCGGCCGGCCCGCCGCCGACGAGGCGGAGCTGACCGCCGCGACCCGGGCGGCCGGCCTG
      >V  F  H  A  T  V  R  E  N  L  L  L  G  R  P  A  A  D  E  A  E  L  T  A  A  T  R  A  A  G  L
95264 CTGGACTGGGTGCACGCCCAGCCGGCCGGGTGGGACACCGTGGTCGGCGAGGAGGGCGGACAGCTCTCCGGCGGCCAGCGGCAGCGCCTCGC
      > L  D  W  V  H  A  Q  P  A  G  W  D  T  V  V  G  E  E  G  G  Q  L  S  G  G  Q  R  Q  R  L  A
95356 GCTGGCCCGGGCGCTGCTCGCCGCGCCCGGGGTGCTGGTGCTCGACGAGCCGACCGAGGGGCTCGACCCGTCCGCCGCCGACGCGGTGCTCG
      > L  A  R  A  L  L  A  A  P  G  V  L  V  L  D  E  P  T  E  G  L  D  P  S  A  A  D  A  V  L
95448 CCTCGGCGCTGGCGGCGACCCCCGCCGGGCACTCGGTGCTGCTGATCAGCCACCGGCTCAGCGGGCTCGCCGACCTCGACGAGATCGTGGTG
      >A  S  A  L  A  A  T  P  A  G  H  S  V  L  L  I  S  H  R  L  S  G  L  A  D  L  D  E  I  V  V
95540 CTCGACGCCGGCCGGGTGGTCCAGCGTGGCCGGCACGACGAGTTGGTCGCCGCGCCGGGCTGGTACCGGGACCAGTGGCTGCTCCAGGAGGC
      > L  D  A  G  R  V  V  Q  R  G  R  H  D  E  L  V  A  A  P  G  W  Y  R  D  Q  W  L  L  Q  E  A
95632 GGCCGAGCGCGGGTACCTGGCCCTGACGCCCCGCCCCTGAGCCGGCTCCGGGATTCCCCCGGACGCGTCGGCAGTCACCGCATGGCAGGCT
      > A  E  R  G  Y  L  A  L  T  P  R  P  •
95723 CGTCGCATGGTGCGCTGCGACGACGTACTCGTGAAGGAGCGGCTGCGCGAGTTGAGCGACCGGCTGCACGGCCCGGCACGGCTCAAGGCCG
            > M  V  R  C  D  D  V  L  V  K  E  R  L  R  E  L  S  D  R  L  H  G  P  A  R  L  K  A
95814 ACCTGCTGGCCGAGGCCCGCCACGCGTTGCAGGACGCCGTCGAGGCGTACCGGGACGGCGGGCTGCCGGCGGCGGAGGCCGAGCGGCGGGCA
      >D  L  L  A  E  A  R  H  A  L  Q  D  A  V  E  A  Y  R  D  G  G  L  P  A  A  E  A  E  R  R  A
95906 GTGGCCGAGTTCGGCGAGCCGGCCCGGCTCGCCCCGGCGTACCAGGCGGAGCTGGCGGCCGGGTCGCTGCGCGGCCTGTCCCTGCGGGTGCT
      > V  A  E  F  G  E  P  A  R  L  A  P  A  Y  Q  A  E  L  A  A  G  S  L  R  G  L  S  L  R  V  L
95998 CGCGGTCGCCGGCGTCCTGGTCGTCGCGGGCGATCTGACCTGGCAGGGGTCGAGCTGGAGCGGCGGCCCCGGCCCGCCGGCGGCCTACCGCC
      > A  V  A  G  V  L  V  V  A  G  D  L  T  W  Q  G  S  S  W  S  G  G  P  G  P  P  A  A  Y  R
96090 TGCTGTCCGCCTCGGTGGACGGCATCTGGCTGGGCGCGGTCGTGCTGTCGGTGGCGGGGTTGCTGCTGGTCGCCGCCTCGGCCCGGTGGGCG
      >L  L  S  A  S  V  D  G  I  W  L  G  A  V  V  L  S  V  A  G  L  L  L  V  A  A  S  A  R  W  A
96182 CACCCGGCCCTGCCCCGGCTCGCCCGGCTGACCGGTCTCGGGCTCACCGCCACGCTCGTCCTGGGCGTGGCGACCGGCGCGGCCCTGTACGC
      > H  P  A  L  P  R  L  A  R  L  T  G  L  G  L  T  A  T  L  V  L  G  V  A  T  G  A  A  L  Y  A
96274 CTGGTCGATCGGGCTCTGGGAGGCGGCCCGCACCTGGCCGCCGATGCTCGTGGGCGCGCTGGTCTGCGGCGCGGGGTTCTTCTGGATCGGTC
      > W  S  I  G  L  W  E  A  A  R  T  W  P  P  M  L  V  G  A  L  V  C  G  A  G  F  F  W  I  G
                                                                                          junction marker
96366 GGGCGGCCCGGTCCTGGCTGCTCTCGGCACGCCGACCGGCCGGACCGGCGTAGTCGGGTGGGCGGCGGGCGCGGTCAGGCCGGCGTGGCGG
      >R  A  A  R  S  W  L  L  S  A  R  R  P  A  G  P  A  •                                  <  •  A  P  T  A  P
96457 GGGTGTCGCCGAGGAACTGGCCGACGGTCGCGCTGAACTCCCGCCAGCCGGCCCGTTCCCCGGCGAGGGCCCGGCGGCCGGAGTCGGTCAGC
      <  T  D  G  L  F  Q  G  V  T  A  S  F  E  R  W  G  A  R  E  G  A  L  A  R  R  G  S  D  T  L
96549 TCGTAGGTGCGGCGCTCGCGGCCGTTGACGGTGCTCCAACTGCTGACCACGTGCCCCGCCCGCTCCAGCCGGCGCAGCGCCGGGTAGATCGT
      <E  Y  T  R  R  E  R  G  N  V  T  S  W  S  S  V  V  H  G  A  R  E  L  R  R  L  A  P  Y  I  T
96641 CCCGGTAGGCAGATCGAGGCTGCCCTCGCTGCGCGCGCGCAGCGCCTCGATGATGGCGTAGCCGTGCAGCGCGCCCCGTTCCAGCACCGCGA
      <  G  T  P  L  D  L  S  G  E  S  R  A  R  L  A  E  I  I  A  Y  G  H  L  A  G  R  E  L  V  A  L
96733 GCAGCAGCGCGTCGAGGTGTCCGTGCAGCGCCTGGGCCTTCATAGGTAGCAAGACTACTTGTGGGCCACTCGCGCCGCCACCGGGGTGCGG
      <  L  L  A  D  L  H  G  H  L  A  Q  A  K  M
96824 GCACCGGGCCTCCTAAGCCGCCCACTAGGGTATGTGCCCAGAGTCACTCGGCGGCCGGAGACGCCGCCGGGTGGGCAGCCCGAAGCACAC
                                                                                  >  V  G  S  P  K  H  T
96914 GGAGGTCAGCGTGGCCCGCCAGTCGCCCCAACGGCCCGACGCCGACGAGCCTGAGCTCGACGAGACCGACGGCACCGCCGCAGAGGTCGAAG
      >  E  V  S  V  A  R  Q  S  P  Q  R  P  D  A  D  E  P  E  L  D  E  T  D  G  T  A  A  E  V  E
97006 AGGACGGCGCGCGCCCGTCGGCGCAGGACGCCGACCGCGCGCTCTGGGACGAGCTGCGCATCGACCCGGTCGAGATCGCCCTGCCCGCCGGC
      >E  D  G  A  R  P  S  A  Q  D  A  D  R  A  L  W  D  E  L  R  I  D  P  V  E  I  A  L  P  A  G
97098 ACCGGCTACACGCTGCGGGCGTACCGGCCGGCACGGGAGTTGACCCCGACCGACGTCGCCGAGCGCGACCAGGACGACCCGTTCCTGGCCCG
      >  T  G  Y  T  L  R  A  Y  R  P  A  R  E  L  T  P  T  D  V  A  E  R  D  Q  D  D  P  F  L  A  R
97190 CCGGCAGGCGGTCGAGACCGACGAGGACGAGGACGAGGTCATCATCCTCGACGAGGAGGTGGCCGCCGAGTTCGCCGAGGCGGACGCGGAGG
      >  R  Q  A  V  E  T  D  E  D  E  D  E  V  I  I  L  D  E  E  V  A  A  E  F  A  E  A  D  A  E
97282 AGGCCGGCGGGAAGTCCCGCTCCCGCAAGCCCCGCGCCGACGCGGACTCCGACGACGCCGGAGCCGCCACAGACGCGGACGCGGAGGAGGAG
      >E  A  G  G  K  S  R  S  R  K  P  R  A  D  A  D  S  D  D  A  G  A  A  T  D  A  D  A  E  E  E
97374 CCGGACTCCGACGAGGACGAGGCGGGCGACGAGGAGGTTCCGGTCTTCCTCAGCCACCGGGGCAGGCTGCTGCTGTTCAAGACGCCCGAATC
      >  P  D  S  D  E  D  E  A  G  D  E  E  V  P  V  F  L  S  H  R  G  R  L  L  L  F  K  T  P  E  S
97466 CCTCGTCAGCTTCGTCCGGTCCGGCGCACCCAACGACATGTCTCAACTGGACAGCTGGAATGAACTGTCCGAACGGGTGGAGCCGGCCGACA
      >  L  V  S  F  V  R  S  G  A  P  N  D  M  S  Q  L  D  S  W  N  E  L  S  E  R  V  E  P  A  D
97558 TCGTCCCGCTCGACGAGGACACCTACGAGCTGGACCTGGTCGTGGAGAACCTGCGGGGTGGGCACGACACCTGGGACTCGGCGCTGCTGATC
      >I  V  P  L  D  E  D  T  Y  E  L  D  L  V  V  E  N  L  R  G  G  H  D  T  W  D  S  A  L  L  I
97650 GAGCCGGCGAGGTGGCCCGGGACGTCGCGTATGCCCTGCGTCTGCCCGCCGTGTTGGACATGCTCTCCGCCGGCTCCAGCCTCGACGACCTG
      >  E  P  A  R  W  P  G  T  S  R  M  P  C  V  C  P  P  C  W  T  C  S  P  P  A  P  A  S  T  T  W
97742 GACGAGGCGCTGCGCGCCACGGCCAACGGCGGGCTCGGGGGCTTCCTCGGCCGCCGGCGGCTGAGGAAAATCGGCGCGCAGACGGCGAGTC
      >  T  R  R  C  A  P  R  P  T  A  G  S  G  A  S  S  A  A  G  G  •
97833 TCGGTTGGCGCACCATTGTCGGCAAGATCTCTGCGGTCGTGGACTGGCGCGACTGACACGTTCCAGGGAGCATCAGTCTCTGGCAGAGAAAG
                                                                                  BamHI
                                                                                junction marker
97925 ACCAGTCCCGGGAGGAGGACGACGCTGTGGCGCTCGTGCGCGTGTACTGCGGTCTGGCCTCGGCGGATCCGGCCGACCGACCGGCCTCGGCC
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Figure 11Z

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98017 GGTTCGGCGCTGACGTCCGCTGTGGTCGACGACGCAGGTCGGCTGCTCCATGTCTGCGAGATCGGCGACGACCCAGCCGGCTACGCTCAGCT
98109 GGTCGTGCTACTCGTGGAGCGGTCGGGCGGGCCGAGCGGGGCTGCGATCGCCGCCGACAGCGACGACCACACGGTCACCTCGCTGCTGAGTG
98201 CCGCCGGGCGTCCACTGGCGATCGCGGACGACGACTCGGTGGACGACTTCGCCGAGCGGTTCGCCGACGACGACTCGCTGGAGGAGATGCA
                                                                                          > M  Q
98292 GTCCGCGCCGGCCGAGCGGCGGGCGGTCGGGCTGGCCCGGGCGCTCCAGGCCGGCGCGCTCTCGGCGGTCACCCTCCCGGCGCCCCGGGATC
      > S  A  P  A  E  R  R  A  V  G  L  A  R  A  L  Q  A  G  A  L  S  A  V  T  L  P  A  P  R  D
98384 TCGCCGGCTACAAGCAGGTCCTCTCGGCGCACGCCGCGCTCGCCAGCGGCCGGCACTCCGCCGCCGTGGCGCTGCGCGAGGTGCTGCGGGAG
      >L  A  G  Y  K  Q  V  L  S  A  H  A  A  L  A  S  G  R  H  S  A  A  V  A  L  R  E  V  L  R  E
98476 CTCTACCCGGCCGCCCTGCGCGCGTACCCGGACCCGGCCGAGCCGGTCGCCCTGGCCGTGTTGGACGCCCTGCCCGAGCCCGGCATGCTGGG
      > L  Y  P  A  A  L  R  A  Y  P  D  P  A  E  P  V  A  L  A  V  L  D  A  L  P  E  P  G  M  L  G
98568 CGGGACGATCGCCCGGGGCCGGGAGGTGTCGGTGGCGGCGGACGCCATCGCCGCCCACCTCGCGGCCGACGGGGTGGCCGACGAAGGCAAGA
      > G  T  I  A  R  G  R  E  V  S  V  A  A  D  A  I  A  A  H  L  A  A  D  G  V  A  D  E  G  K
98660 TCAACGATGCGGTGACCGCGCTGCGGGTCGCCATCGCCGAGACCCCCCGCCGCGCGGCGGTCAGCCGGGCGCTCACCTCCGCCGTGGCGGAG
      >I  N  D  A  V  T  A  L  R  V  A  I  A  E  T  P  R  R  A  A  V  S  R  A  L  T  S  A  V  A  E
98752 ACGGTCCGTCAGGCGGTGGCCTCGGTGCGAGCATGCGACGCGGGCTGCGAGGCCCTGGTCGGCGCGCTCGACGCCCGGGTCACCACCCCCAC
      > T  V  R  Q  A  V  A  S  V  R  A  C  D  A  G  C  E  A  L  V  G  A  L  D  A  R  V  T  T  P  T
98844 CCCGGTGCCGGGCCGGCGGGCCGCCGCCCGCCGGGGCGAGCCGGTCGCCGAGTTGCCCGGCGCCGGCCTGCGCGCACTGCGGCCCACAGAGC
      > P  V  P  G  R  R  A  A  A  R  R  G  E  P  V  A  E  L  P  G  A  G  L  R  A  L  R  P  T  E
98936 CCGAGCCGGTCCCCGGCCGGCGCAGCCGTCCCGAGCCGGTCCCCGGCGGCAGCCTGCCCGCCCAGCCCCGCCCGCTCGGCCCGCCGCCGGTC
      >P  E  P  V  P  G  R  R  S  R  P  E  P  V  P  G  G  S  L  P  A  Q  P  R  P  L  G  P  P  P  V
99028 GCGCCGGAGCCCGTCGCCCCGCCGCCGGTCGCCCCGCGCCCGATCACCCCGGCCGCCTCGGCCACCCCGCCGGTCTCCGGCCCGCCGTCGCC
      > A  P  E  P  V  A  P  P  P  V  A  P  R  P  I  T  P  A  A  S  A  T  P  P  V  S  G  P  P  S  P
99120 CGAGCCGCGCCGCCTGATCGACAACCCGGCCAACCGGCCGGTCTCCGCGCCGCCGCCCCCGCCACCGGGGATCACCCCGATCGCGCCGAGCC
      > E  P  R  R  L  I  D  N  P  A  N  R  P  V  S  A  P  P  P  P  P  P  G  I  T  P  I  A  P  S
99212 AGCGCGAGCGCGGGTCCGTGCCGCCGGCCGAGGCCGGTGAGCCGTTCCGGCCCACGCTGACCACCGCCGCGATCCAGAACGCGCGGGCGGAG
      >Q  R  E  R  G  S  V  P  P  A  E  A  G  E  P  F  R  P  T  L  T  T  A  A  I  Q  N  A  R  A  E
99304 CGGCAGCGCACCATCATCCCGCCTCGCCCCAAGACGACGGGCGAGTCCGCGCCGCCGCCCACCGGCGGCTTCAGCGCCACCGACCTGAGCGT
      > R  Q  R  T  I  I  P  P  R  P  K  T  T  G  E  S  A  P  P  P  T  G  G  F  S  A  T  D  L  S  V
99396 CCCGGTGCCGACCCCGCGTCCCGGCCAGGAGTCCGCTCCCCCCGGCTCGCGGGCGAACTGGCCGCTGGTCAACAACCCCGAGGACCCCGCCG
      > P  V  P  T  P  R  P  G  Q  E  S  A  P  P  G  S  R  A  N  W  P  L  V  N  N  P  E  D  P  A
99488 ACAGCTCCCCGAACAATCCCGTCGCGCGGCGGCCCTTGGAGGATCGGGCGAAGCGGCAGATCGACGCGCCGACCCAGGTGGTCCCGCCGGCC
      >D  S  S  P  N  N  P  V  A  R  R  P  L  E  D  R  A  K  R  Q  I  D  A  P  T  Q  V  V  P  P  A
99580 GAGGGCCGGGTCACCCCGCCCTGGCTCGCCGACGACCTGCCCCAGGAGCCACCGATGCTGCGGCTGGTCGAGCCGCCACCGCTGGCCGACCG
      > E  G  R  V  T  P  P  W  L  A  D  D  L  P  Q  E  P  P  M  L  R  L  V  E  P  P  P  L  A  D  R
99672 GGCACTGCGGGATGGGCCGGGCCAGGCTGCCGACCCGCGCCTGGAGCCCCCGCCGCTGCGGCTGGTCGACCGCGGCGAGGCAGCCCGCGCCG
      > A  L  R  D  G  P  G  Q  A  A  D  P  R  L  E  P  P  P  L  R  L  V  D  R  G  E  A  A  R  A
99764 GCCGTCCCGCGCCGGAGCCCCGCCCCGAGCGGGCCCCCGCGGAACACCGGTCCCCGCTGGGTCAGCGGGTCCCGTTGGAGGAGCGGCCCGAC
      >G  R  P  A  P  E  P  R  P  E  R  A  P  A  E  H  R  S  P  L  G  Q  R  V  P  L  E  E  R  P  D
99856 ATGGAACATCGGACCGCCCCGCCGCAGCCGTCGCGGTCCGCGCCGATGGAGCGGCGTACCCCGCCGATCTCCGACGAGGGGGACGGCGACCT
      > M  E  H  R  T  A  P  P  Q  P  S  R  S  A  P  M  E  R  R  T  P  P  I  S  D  E  G  D  G  D  L
99948 GCTGATCTTCGCCGCCGCCAAGTCGGCCTGGTTCGTCGGGCACGGCGACGAGTCCGAGATGGACTGGTCGAGCACCGCCGACACCGGGTGGC
      > L  I  F  A  A  A  K  S  A  W  F  V  G  H  G  D  E  S  E  M  D  W  S  S  T  A  D  T  G  W
100040 AGGCCGCCGAGCAGGCCGCCCGCCCGGCGGTGGGCGCCGATACCAAGGCCGGGTTGCCCAAGCGGGTGCCGCAGGCCAACCTGGTTCCGGGC
      >Q  A  A  E  Q  A  A  R  P  A  V  G  A  D  T  K  A  G  L  P  K  R  V  P  Q  A  N  L  V  P  G
100132 TCCCCCCTGCGCGAGGAGCGTCCCCTACGGATAGTCCGCGACGCGGCCAGCCTCGCCGAGAACACGACCGGCTACTTCCGGGGCTGGCGTCG
      > S  P  L  R  E  E  R  P  L  R  I  V  R  D  A  A  S  L  A  E  N  T  T  G  Y  F  R  G  W  R  R
100224 CGGGCAGGAGATCGGCGGGTTCGCCGTCGGCGGCCGGCCGGGCCGCGAGGCGGCCGGCGGCTGGGACTTCACCCGGGACACCGGCGACCGAG
      > G  Q  E  I  G  G  F  A  V  G  G  R  P  G  R  E  A  A  G  G  W  D  F  T  R  D  T  G  D  R
100316 ACGACGACCGGGAGTACGAGTACCGGTCCGCCGGCTACCGCTCCTGACCATCGCGCCGGGGTGGCGGGCACCGCCGCCCCGGCCGCGCCCG
      >D  D  D  R  E  Y  E  Y  R  S  A  G  Y  R  S  •
100407 CCGTGCTGGCGTACGGCCGTAGCAACCCGACGCCCACCCGACCGACCGGTGGGACCACACCGAAGAGCAACCCTGGCCGGCCGCCTGACGTC
100499 CCGCAGGGACGGTGACGGCTACTGGCCGTCCCCCCGGGAAGGTTGCGAGGCGGTCGGGGCGCACAGGCGCTGTCAGGGCCGCTCCTGAGCCG
100591 CCCTACGGAATGGGCTAGCCCTACGGAATCGAGCGCCGGCCGCCCGCCGGTGGCGTCGAGTTCGCCTCCAGCCGGTCCCCAAACAGCCGGAC
100683 GCGCCCGACGGCCCGGCGGGTGCCGGTCGTCGGGCGCGTCCCGTCGTCGATCAGGCCGGCGCGACCGCGCGCGAGCGGCGCATCGTGAGCA
                                                                                  < •  A  P  A  V  A  R  S  R  R  M  T  L  V
100774 CGTACTCGACCAGCGAGATCAGCACGTGCTTCGTCGACTCCCGGTTCCGGGCGTCGCAGGCCACCACCGGCACGTCGTGCGAGATCGCGAGC
      < Y  E  V  L  S  I  L  V  H  K  T  S  E  R  N  R  A  D  C  A  V  V  P  V  D  H  S  I  A  L
100866 GCGTCCCGGACGTCCTGCGGGTCGTGGTACTGCATCCCGTCGAAGCAGTTGATGGCCACCAGGTACGGCAGCCGCCGATGCTCGAAGAAGTC
      <A  D  R  V  D  Q  P  D  H  Y  Q  M  G  D  F  C  N  I  A  V  L  Y  P  L  R  R  H  E  F  F  D
100958 GATGGCCGCGAAGCAGTCGGCCAGCCGCCGGGTGTCGACCAGGACCACCGCGCCGATGGCGCCCCGGACCAGCTCGTCCCACATGAACCAGA
      < I  A  A  F  C  D  A  L  R  R  T  D  V  L  V  V  A  G  I  A  G  R  V  L  E  D  W  M  F  W  F
101050 ACCGGGTCTGGCCGGGGGTGCCGAACAGGTACAGGATCAGGTCCCGGTCGATCGAGATACGGCCGAAGTCCATCGCCACCGTGGTCGTCGTC
      < R  T  Q  G  P  T  G  F  L  Y  L  I  L  D  R  D  I  S  I  R  G  F  D  M  A  V  T  T  T  T
101142 TCGCCCGGCACCTGCCGGGTGTCGTCGACGCCCACGCCGGCGGAGGTCATGATCGCCTCGGTGGTCAGCGGCGTGATCTCCGAGACCGAGCC
      <E  G  P  V  Q  R  T  D  D  V  G  V  G  A  S  T  M  I  A  E  T  T  L  P  T  I  E  S  V  S  G
101234 GACCAGCGTCGTCTTGCCGACGCCGAACCCACCGGCGATAACGATCTTCGCCGACGTCACGCGCCCGCTCGGGACAGGCGGGCGGTGCGACA
      < V  L  T  T  K  G  V  G  F  G  G  A  I  V  I  K  A  S  T  V  R  G  S  P  V  P  P  R  H  S  M
101326 TGTCAGAGCCTGCGAAGTCCACTCAGCACCCTCTCCAGCAGTTCAGTGCCCACCGCGTCGTCGGAGTCGTCCAGGATGGTCGGCTCGTGGA
      < < •  L  R  R  L  G  S  L  V  R  E  L  L  E  T  G  V  A  D  D  S  D  D  L  I  T  P  E  H  V
101417 CTGCGACCAGGCCGTCGTCGCCATGTCGGCGATGAGCACCCTAGCCACGCCGAGCGGGAGCTGCATCCGCGGCCGCGATCTCGGCAAGCGAC
      < A  V  L  G  D  T  A  M  D  A  I  L  V  R  A  V  G  L  P  L  Q  M  R  A  A  I  E  A  L  S
101509 TGCACGCGTCCGTCGCACAGCGCGGCGATGTACTGGTGCTCTCGGCCCTGGCCACCGTTGCTACTGGCAGCGGCCCGACCGCGCACCGTCGT
      <Q  V  R  G  D  C  L  A  A  A  I  Y  Q  H  E  R  G  Q  G  G  N  S  S  A  A  A  R  G  R  V  T  T
101601 CTCGACGAGCGCCTCCAACGCGATGTCCAGCCGAGGGCGGGTACGACCGCGGGTGACGGCGTACGGACGGACCAACGCGCCAGTCGGCTCGT
      < E  V  L  A  E  L  A  I  D  L  R  P  R  T  R  G  R  T  V  A  Y  P  R  V  L  A  G  T  P  E  D
101693 CACGATCCATGTCGCCGCTCACCTCCTTCGTCCCCGACACCGGCTGAACCCGGTGGAACCCGTCGTTCTTGTCCTTGCCACCCCGCCCGAC
      < R  D  M  D  G  S  V  E  K  T  G  S  V
101784 CCATCGGCCAGCGCGTGGGTCAGCCCATCATCCCCACAGTCGTACGCGGCTGCGGGGTCAACGCGTCGCCCACCCGGTCGACCAGGAGGGC
                                                  < •  G  M  M  G  V  T  T  R  P  Q  P  T  L  A  D  G  V  R  D  V  L  L  A
```

Figure 11AA

```
101875 CATCTCGTATCCGACCTGCCCGACGTCGCAGCTACGGGCGGCGAGCACGGCGAAGGACGAGCCGTCCGAGATGGACATCAGGAACAGGAAGC
      < M  E  Y  G  V  Q  G  V  D  C  S  R  A  A  L  V  A  F  S  S  G  D  S  I  S  M  L  F  L  F  G
101967 CGTTGTCCATCTCGACCACGGTCTGCAGCACCGCACCGCCCTCGAAGCAGCGTGCCGCTCCCTGCGTGAGGCTGACCAGCCCGGACGCGATC
      < N  D  M  E  V  V  T  Q  L  V  A  G  G  E  F  C  R  A  A  G  Q  T  L  S  V  L  G  S  A  I
102059 GCGGCGAGCTGGTCGGCCCGGTCACGCGGAAGGTCTCGTGACGACGCCAGGAGCAGACCGTCCGCGGAGACGGCGACCGCGTGCGCGACACC
      <A  A  L  Q  D  A  R  D  R  P  L  D  R  S  S  A  L  L  L  G  D  A  S  V  A  V  A  H  A  V  G
102151 GGGCACCCGGTCGGCGAAGTTGGCCAGCAGCCAACCGAGATCCTGCGTAGTTGTCATCCTTGTTGCTCCTTCTGCCCGCTCCCGGCCACCG
      < P  V                                                  <  •  G  Q  Q  E  K  Q  G  S  G  A  V  P
102242 GGCCTGAGCCAGACTGCGAGGATTGCTGCCCACCCGGAGCTGCCTCCGGGTTGGTCGGGTTGCCGTCGGGCTCGGTACGCCCACGCTGCACG
      < G  S  G  S  Q  S  S  Q  Q  G  G  P  A  A  E  P  N  T  P  N  G  D  P  E  T  R  G  R  Q  V
102334 CCTCGATGGTATGCCGAGAGCAGACCGCGGACGCCCTCCGGCGTACGGCGCTGGACCGACGTGGTGGGCTTCTCCACCCCGCCAGGCACGAG
      <G  R  H  Y  A  S  L  L  G  R  V  G  E  P  T  R  R  Q  V  S  T  T  P  K  E  V  G  G  P  V  L
102426 TTGGGCCATCGGCACCCGCTTCGGCAGGCCCTTGCGGGTGGTCTCCGCCACCGGGACCTCGGTGGCCGCCGAGGCGGCCCGCCAGCCGTCGT
      < Q  A  M  P  V  R  K  P  L  G  K  R  T  T  E  A  V  P  V  E  T  A  A  S  A  A  R  W  G  D  D
102518 CCGCGGCAGTCTGCCAGGCGTGGGCCTGCGGCGTGGGCCGCCGGCCGGCGAAGCCCTCGGCGGGACCGGGGCGGGTGCCACCGTTGGTCGGC
      < A  A  T  Q  W  A  H  A  Q  P  T  P  R  R  G  A  F  G  E  A  P  G  P  R  T  G  G  N  T  P
102610 GACCCGTTGTCGCGCGGCATTCCTCCGGCCATCGGGGTGTCTGCCATCGGTGCGTTACCTGTCGTCCCGGGTGCTGGTGTCTGGACGGGCCG
      <S  G  N  D  R  P  M  G  G  A  M  P  T  D  A  M  P  A  N  G  T  T  G  P  A  P  T  Q  V  P  R
102702 GCCGGTGACGTCGACCGCGGAGAACTGTTGGGTCACGGCGGCGTTCGCCGGGCTCCCGGCGCCATTGGTCGCGCGCTGGGCGACGCCGGCCG
      < G  T  V  D  V  A  S  F  Q  Q  T  V  A  A  N  A  P  S  G  A  G  N  T  A  R  Q  A  V  G  A  T
102794 TCTCCTCCGAACCCGAGCGGCGGGTACGGAACCAGGCCGACTCGAGCTCCCGGAAGATCGGCAGCTCCATCGTCTCGTCCGCGTACCGCTGC
      < E  E  S  G  S  R  R  T  R  F  W  A  S  E  L  E  R  F  I  P  L  E  M  T  E  D  A  Y  R  Q
102886 TGCCGGTTCTGGGCCTGCACGGGCGTCGACCGCGCCGGCGTGGGCGGGGTCGTCGGCTGGGTGGCCGGCGTGCTCGGCACCTCGGTGCTCGG
      <Q  R  N  Q  A  Q  V  P  T  S  R  A  P  T  P  P  T  T  P  Q  T  A  P  T  S  P  V  E  T  S  P
102978 CACCCGGGGCAGCTCCGTGGTCATGTCCAGGGCTGCGGCGAGGCGCTCCGGCACCGGCGGGGTGACCGGCTCCGGCGCGGCCACCGGCGGCC
      < V  R  P  L  E  T  T  M  D  L  A  A  A  L  R  E  P  V  P  P  T  V  P  E  P  A  A  V  P  P  W
103070 AGGCCGGCGGCGCCACGGGCGCCTGGGCCGACGGGACCGGCCGACTGGGCAGCGGCTGCGCCGAGTACGGCTGACCGGACACGGGCGTGCCG
      < A  P  P  A  V  P  A  Q  A  S  P  V  P  R  S  P  L  P  Q  A  S  Y  P  Q  G  S  V  P  T  G
103162 AACGGCTGACCGGAGACGGGCGTGCCGAACGGCTGACCGGACACCGGGGCGGCCGAGACGGGCTGACCCGAGACCGGGAAGACGGAAACCGG
      <F  P  Q  G  S  V  P  T  G  F  P  Q  G  S  V  P  A  A  S  V  P  Q  G  S  V  P  F  V  S  V  P
103254 CGGTGCGGACACCGGCGGCACCGAGACCGGTGGCGGGGTCCAGCCCCGGGCCTCCGGGCTGCTCGGCAGCTGTCGGGGGATGGCCGGCTGCT
      < P  A  S  V  P  P  V  S  V  P  P  P  T  W  G  R  A  E  P  S  S  P  L  Q  R  P  I  A  P  Q  Q
103346 GGCCGCTGCTGGCCGGATCGCCGTCGCCGGACGCCCGCCGCTGCGGCAGCGGGTCGCTCGACTGGCCATTCGAGGTGCGGCCGGCGGCGGCA
      < G  S  S  A  P  D  G  D  G  S  A  R  R  Q  P  L  P  D  S  S  Q  G  N  S  T  R  G  A  A  A
103438 CCGCCAGCGGTGCCACTGGCCCCGGTCAGGTCCGACCAGGCCGGCATCGACCGCATGGAACCGGTCGACGCGGGCGTGCCGTGGCCGTTGCG
      <G  G  A  T  G  S  A  G  T  L  D  S  W  A  P  M  S  R  M  S  G  T  S  A  P  T  G  H  G  N  R
103530 CGAGGCCGGGTCGAACGACCGGCCGCCCAGGGTTACCTGGTTGCCCGAGTGCCCCGGCCGCTGGGTGGGCGCCGGTGTCGCCGGGTTGTTGC
      < S  A  P  D  F  S  R  G  G  L  T  V  Q  N  G  S  H  G  P  R  Q  T  P  A  P  T  A  P  N  N  G
103622 CGAAGGCCGCGAAGGCACCCAGGGCCGGGGGGGCCCCGCCGGGCTGCGAGCTGGTGAGCGAGGCGGGAGGGGCCGGCAGCGCGCCGGGCTGC
      < F  A  A  F  A  G  L  A  P  P  A  G  G  P  Q  S  S  T  L  S  A  P  P  A  P  L  A  G  P  Q
103714 TGGAACCGGCCGGAGAGCGCCCGGGGCACCAGCACGGTGGTGGGCAGGGTGACGTCGGCGACGGTCCCCCGGTCGGTGCCGGGCCGCAGCTC
      <Q  F  R  G  S  L  A  R  P  V  L  V  T  T  P  L  T  V  D  A  V  T  G  R  D  T  G  P  R  L  E
103806 GACCTTGACCCCGTGCCGGGACGCCAACCGGGCGACCACAACCAGGCCCATCATCCGGGAGACGGCCACGTCCACCTGCGGCGGCGAGGCGA
      < V  K  V  G  H  R  S  A  L  R  A  V  V  V  L  G  M  M  R  S  V  A  V  D  V  Q  P  P  S  A  L
103898 GGCGGTCGTTGAGGTCGTGTAGCTGCTCGGCGCTGATGCCGATGCCCCGGTCCTCGACGTAGAGGTTGGCCCGGTCGCCGACCCGGCGGGCC
      < R  D  N  L  D  H  L  Q  E  A  S  I  G  I  G  R  D  E  V  Y  L  N  A  R  D  G  V  R  R  A
103990 TCCACCATCACCTGCGAGTCGGGCGGCGAGAAGGCGGTCGCGTTGTCGAACAGCTCGGCGACCAGGTGGACCAGGTCGTTGACCGCGTGCGC
      <E  V  M  V  Q  S  D  P  P  S  F  A  T  A  N  D  F  L  E  A  V  L  H  V  L  D  N  V  A  H  A
104082 GGCGACCTCGATGTCACGGTCGATCACCCCGAACTCGATCCGGGTGTAGTGCTCGACCTCGGACTGGGCGGCCCGCAGCACGTCGATCAGTG
      < A  V  E  I  D  R  D  I  V  G  F  E  I  R  T  Y  H  E  V  E  S  Q  A  A  R  L  V  D  I  L  A
104174 CCGCCGGCTCGCGCTGCACGCGGGTGGAGTCGGCCCCGGCGAGCACCAGCAGGTTCTCGTCGTTGCGGCGCATCCGGGTGGCCAGGTGGTCG
      < A  P  E  R  Q  V  R  T  S  D  A  G  A  L  V  L  L  N  E  D  N  R  R  M  R  T  A  L  H  D
104266 AGCTGGAACAGCTCGGCCAGCCGGTCCGGGTCCTCCTCGCCGCGCTCCAGCCGGTCGAGGTGGCCGATCAGCCGGTCGACCAGGATCTGCGA
      <L  Q  F  L  E  A  L  R  D  P  D  E  E  G  R  E  L  R  D  L  H  G  I  L  R  D  V  L  I  Q  S
104358 ACGGCGGGCCAGGTTGACGAACATGGTCGCGACGGAGGCGCGCAGCGCGGCCTGCTCCGCCGCCGTCCGTACGGCCTCCAGGTGGACCGCGT
      < R  R  A  L  N  V  F  M  T  A  V  S  A  R  L  A  A  Q  E  A  A  T  R  V  A  E  L  H  V  A  N
104450 TGAACGCCTCGGTCACCTGGCCGAACTCGTCCTTGCTGCGCACCGGCAGCGGCTCGGCGATCTGGTTGGCCGCCTGCACCGGGGAGAGCTGG
      < F  A  E  T  V  Q  G  F  E  D  K  S  R  V  P  L  P  E  A  I  Q  N  A  A  Q  V  P  S  L  Q
104542 CTGGAAAACTGCGGATCGCGACAGCCGGGCAACGGCCTGGGGCAAACCGTACTGGGCGATGCTGAGCGCACCCTGGCGCAGGTCGCGCAGCGA
      <S  S  F  Q  P  D  R  L  R  A  V  A  Q  P  L  G  Y  Q  A  I  S  L  A  G  Q  R  L  D  R  L  S
104634 GCGGGCCATCGACCGGGCGACCAGGTACGCGAACAGGATGGCCAGCAGCAGCATGCCGAGCAGCAGGCCGGTCTGGAGGAACACCGTGCGCT
      < R  A  M  S  R  A  V  L  Y  A  F  L  I  A  L  L  L  M  G  L  L  L  G  T  Q  L  F  V  T  R  Q
104726 GTACGTCGGAGCGGAGCGCGTCGGCCTGCTTGACCACGTTGCCGTCGAGCTTCGCCTCGACCGTACGGATCAGTTTGGCGCTGGCGACCATG
      < V  D  S  R  L  A  D  A  Q  K  V  V  N  G  D  L  K  A  E  V  T  R  I  L  K  A  S  A  V  M
104818 GCCGCGTCCCACTGATCCGGCCCGAACGGCGCGTTGGCCATGCTGCCGTTGGTGTTGCCGTCGAGCCAGCCGGTGTAGTTCTGCGCCTCGCG
      <A  A  D  W  Q  D  P  G  F  P  A  N  A  M  S  G  N  T  N  G  D  L  W  G  T  Y  N  Q  A  E  R
104910 CCGGTCGCCGCCGGCGACGGTCTGGTCGTCGCAGGTCCGACTCGTCCAGGCTGGCCACCGCCTTGAAGCTTTGCAGTGCCTGCTGCTGGCCGG
      < R  D  G  G  A  V  T  Q  D  H  L  D  S  E  D  L  S  A  V  A  K  F  S  Q  L  A  Q  Q  Q  G  T
105002 TGCCGCTGGCGATGTAGTCGGTGCGCAGGATGGGGGTCAACTCGCGCTGGATCAGCGCCCGGTGCACCACGACCCGGCGGACCGAGAGGTAT
      < G  S  A  I  Y  D  T  R  L  I  P  T  L  E  R  Q  I  L  A  R  H  V  V  V  R  R  V  S  L  Y
105094 TCCTTCTCCCGGGCGACGGCTGCCGCGGCCCGCATCCGGTCGCTCAGGTCGTTGTCACCGGCGAGGTGGGTGGCGGAGTCGCGGATGGACAG
      <E  K  E  R  A  V  A  A  A  A  R  M  R  D  S  L  D  N  D  G  A  L  H  T  A  S  D  R  I  S  L
105186 CAGGTCGTTGATCAGGCCCTCGTACGCCTGCATGGCGTCGATGATCTTCAACTTGCCGTTGAAGACCTGGCTGCGGGTGCCGGGGAGGTCCT
      < L  D  N  I  L  G  E  Y  A  Q  M  A  D  I  I  K  L  K  G  N  F  V  Q  S  R  T  G  P  L  D  K
105278 TCAGGTTCTGGTCGATCCCGTCGAGGAGGCCCTCCAGGCTGCTCGGCAGGCCGTCGACCTCCCCCCGCTGTTGCAGGTACGGCACCTTGTCC
      < L  N  Q  D  I  G  D  L  L  G  E  L  S  S  P  L  G  D  V  E  G  R  Q  Q  L  Y  P  V  K  D
105370 TGGTCGACCCGGATGTTGACCCGGTTGTACGCCTCCTGGTACTGCGCCTTGGCCTGGTCGCCGCTCGCCCCGAGCAGCAACACCGCGGAGGT
      <Q  D  V  R  I  N  V  R  N  Y  A  E  Q  Y  Q  A  K  A  Q  D  G  S  A  G  L  L  L  V  A  S  T
```

Figure 11AB

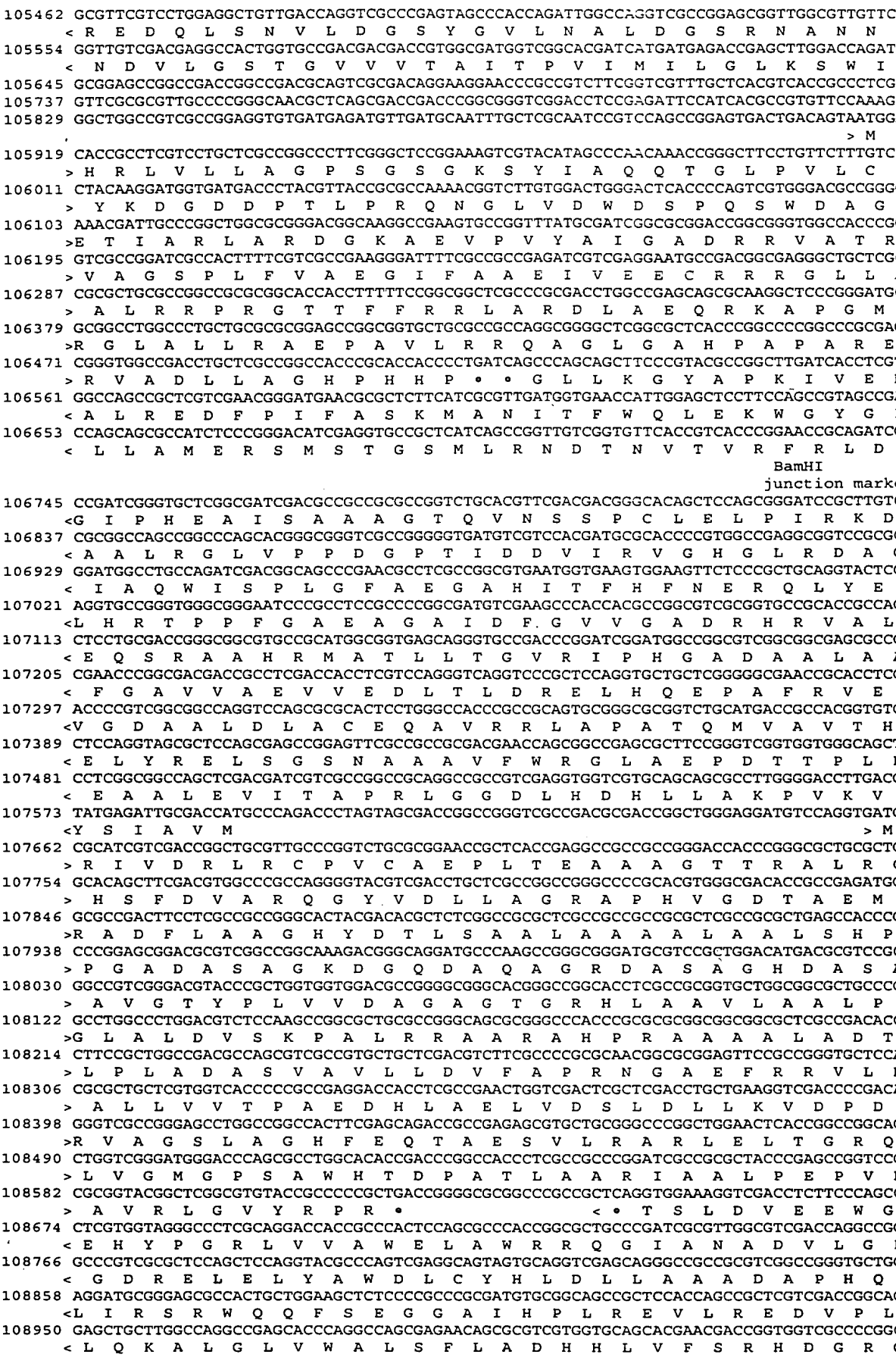

Figure 11AC

```
109042 CGAACTGCCACTCCGGCGGGGTGACCAGGTCGACCAGGTGGGAGTTGAGCAGCCAGCTCATCGCCGCCTGCGCCGGCATGCCGAAACACCGG
       <  F  Q  W  E  P  P  T  V  L  D  V  L  H  S  N  L  L  W  S  M  A  A  Q  A  P  M  G  F  C  R
109134 GCCAGGATCACGTGCAGCACGGCGATGCGCGCCTCGATCTCGACGGTCGGCCGCAGCTCGATCTCGTCGCCCGGCTCCCACACCAGGGGAA
       <A  L  I  V  H  L  V  A  I  R  A  E  I  E  V  T  P  R  L  E  I  E  D  G  P  E  W  V
109225 ACTGGCTCGGTGGCAGCGGCAGCCCCAGCCGGGACAGCTCGTCCAGGCTGGCGTCACGGACCTCTCGCGGGTCGGGAGCGGAAACGCGCACG
109317 GCTCAGATCCCTGTCAGTCGCATCGGCTCAGTGCCGGTCGTCCCCCTTGGCCTGGGAGGATAGCGGTTCACGACGAGCGGCACCACGGCGGG
109409 CGGGGGCGGGGGCGGTTCAGCCGATCCGCTCGATGACCAGCGGCTGCGGGGTCGGGGCGGTCGGCGAGATCCGTACCGCCCGGACCGCCTCG
                     BamHI
109501 GCCAGCGCCGCCGGGATCC
```

Figure 11AD

```
   1 GTCTTCGGGGAACGCCACGGGAACCTCCTCGCCAGAACCGGACGAGCTGACCGTAACCGGTGGGCACCCGCGCGCGGATCAACCGGTGCGGTGGTTCCCAGGTTCCGGCCGCGCGGCCCCG
 122 ACGCACCGCCCCCGGTGTGAGAAGGGGACCCATCTCTACCGTAGGCGTTAACAAGGGGCCCTTCCTT TCA CCG CAG GTG CAG GAC GTC TCC TGC GGC GAG GGT GCG
                                                                    <  •  R  L  H  L  V  D  G  A  A  L  T  R
 228 CGG GCC CGC CCG GGT GTC GAC CAG CAG CCG GCC GTC GGC GTC CAC GCC GGT CGC CAC GCC GGT CAC CTC CGC ACC GCC GGG CAG CAG CAC
    <  P  G  A  R  T  D  V  L  L  R  G  D  A  D  V  G  T  A  V  G  T  V  E  A  G  G  P  L  L  V
 318 CCG CAC CGG TCT GCC GAC CGT CGC GCA GGC CGC CAG GTA CGC GTC GCG CAG CCC GCT GGC CAC CGC GTC GCC GCC GGC GTG GCG CCA GCG
    <  R  V  P  R  G  V  T  A  C  A  A  L  Y  A  D  R  L  G  S  A  V  A  D  G  G  A  H  R  W  R
 408 GTC GTA CCA GTC GGC GAC AGA GCG CAG CAG TGC GCG CAG CAG CGG GTC CCG GTC GGT GGC GAC GGC CCC GGC GAG CTG GAG CGA GGT GGC
    <  D  Y  W  D  A  V  S  R  L  L  A  R  L  L  P  D  R  D  T  A  V  A  G  A  L  Q  L  S  T  A
 498 CGG CAG GCC GGT CGG GTT CGC CGG CAG CTC GTC GGC GCG CAG GGT GAC GTT GAG ACC GAT GCC GAG GAC GAT CGC CGG GGG CTG GTC CGG
    <  P  L  G  T  P  N  A  P  L  E  D  A  R  L  T  V  N  L  G  I  G  L  V  I  A  P  P  Q  D  P
 588 GGC CGG GCC GGG CAC CGC CTC GGC CAG GAT GCC CGC GCA CTT GGC GTC GCC GAT CAG CAG GTC GTT GGG CCA CTT GAG GGC GGC GTC CAG
    <  A  P  G  P  V  A  E  A  L  I  G  A  C  K  A  D  G  I  L  L  D  N  P  W  K  L  A  A  D  L
 678 CTC GGC CAG CCG GGC CAC CGC CTC GAC CAG CGC GAC GCC GGC GAG CAG GGG CAG CCA GCC GTA CCC GGT CGC GGG GGC CGG CGG CCA GTC
    <  E  A  L  R  A  V  A  E  V  L  A  V  G  A  L  L  P  L  W  G  Y  G  T  A  P  A  P  P  W  D
 768 GCG CTC CGC GAC AGC CTC GCC CGG CCG CAG CAG CAC GCT GGT CGC GAT TCC GGC GCG GGG CGG CGA CTG CCA GAC CCG GCC GCG CCG GCC
    <  R  E  A  V  A  E  G  P  R  L  L  V  S  T  A  I  G  A  R  P  P  S  Q  W  V  R  G  R  R  G
 858 CCG GCC GGC GGT CTG CCG CTC GGC GAT CAC CAC GAG GCC CTC CGG CTC GCC GGA TCG GGC CGC CTC CGC CAC GTC CGC GTT GGT CGA GCC
    <  R  G  A  T  Q  R  E  A  I  V  V  L  G  E  P  E  G  S  R  A  A  E  A  V  D  A  N  T  S  G
 948 GGT CTC GGC GCG TAG CTC CAG CCG GGC CCA GGG GCC GTG CGG GGC GGT CAG CGC CCG GCG CAG CCG GGC CGC CGA CAG CGG CGG GCG ATC
    <  T  E  A  R  L  E  L  R  A  W  P  G  H  P  A  T  L  A  R  R  L  R  A  A  S  L  P  P  R  D
1038 CAG GTC GGT GTA CGG CGA GCC GGG CAT CCCGCCAGCCTACGGCCCGCCCGGACGCGGCGGCGGGTGCCGGCGTTGCCCGAGCCCGGTGAGGTTGCTGA GGC GTA CTG
    <  L  D  T  Y  P  S  G  P  M
1145 CAC ACC GTC GGC CAC CTG AAC CAT CGT TAT ATT CCG TGG GTG ACT ACC GAG ACC GGG ATC AAC ATC CAC AGC ACG GCG GGC AAG CTG GCG
                                                          >  V  T  T  E  T  G  I  N  I  H  S  T  A  G  K  L  A
1235 GAC CTG GAG CGA CGG GTC GAC GAG GCG GTG CAC GCC GGA TCG GCG CGT GCG GTG TCC AAG CAG CAC GCC CGG GGC AAG AAG ACG GCG CGG
    >  D  L  E  R  R  V  D  E  A  V  H  A  G  S  A  R  A  V  S  K  Q  H  A  R  G  K  K  T  A  R
1325 GAG CGG ATC GGG CTG CTG CTC GAC GAG GGG TCC TTC GTC GAG CTG GAC GGG TTC GCC CGG CAC CGG TCC ACC AAC TTC GGC CTG GAC CGC
    >  E  R  I  G  L  L  L  D  E  G  S  F  V  E  L  D  G  F  A  R  H  R  S  T  N  F  G  L  D  R
1415 ACC CGC CCG TAC GGC GAC GGG GTG ATC ACC GGC TAC GGC ACG GTC GAC GGG CGG CAG GTC TGC GTC TTC GCG CAG GAC TTC ACG GTC TTC
    >  T  R  P  Y  G  D  G  V  I  T  G  Y  G  T  V  D  G  R  Q  V  C  V  F  A  Q  D  F  T  V  F
1505 GGC GGC TCC CTC GGC GAG GTG TTC GGC GAA AAG ATC GTC AAG GTG ATG GAC CTG GCC ATG AAG ATC GGC TGC CCG GTC GTC GGC ATC AAC
    >  G  G  S  L  G  E  V  F  G  E  K  I  V  K  V  M  D  L  A  M  K  I  G  C  P  V  V  G  I  N
1595 GAC TCC GGC GGC GCC CGC ATC CAG GAG GGC GTG GCG TCC CTC GGG CTC TAC GGC GAG ATC TTC TTC CGC AAC GTG CGG GCC AGC GGC GTC
    >  D  S  G  G  A  R  I  Q  E  G  V  A  S  L  G  L  Y  G  E  I  F  F  R  N  V  R  A  S  G  V
1685 ATC CCG CAG ATC TCC CTG ATC ATG GGC CCG TGC GCG GGC GGC GCG GTC TAT TCT CCG GCG GTC ACC GAC TTC ACC GTG ATG GTC GAC CAG
    >  I  P  Q  I  S  L  I  M  G  P  C  A  G  G  A  V  Y  S  P  A  V  T  D  F  T  V  M  V  D  Q
```

FIGURE 12A

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1775 ACC TCG CAC ATG TTC ATC ACC GGC CCC GAC GTG ATC AAG ACG GTC ACC GGC GAG GAC GTC GGG ATG GAG GAA CTG GGC GGT GCC CGC ACC
    > T   S   H   M   F   I   T   G   P   D   V   I   K   T   V   T   G   E   D   V   G   M   E   E   L   G   G   A   R   T
1865 CAC AAC GCG CGC AGC GGC AAC GCG CAC TAC CTC GGC ACC GAC GAG GAG GAC GCG ATC GAG TAC GTC AAG GCG CTG CTG TCG TAC CTG CCG
    > H   N   A   R   S   G   N   A   H   Y   L   G   T   D   E   E   D   A   I   E   Y   V   K   A   L   L   S   Y   L   P
1955 TCG AAC AAC CTG GAC GAG CCG CCG GTC TTC GAC GCC CCG GCC GAC GTG GCG ATC AGC GAC GCC GAC CGG GAG CTG GAC AGC CTC GTC CCG
    > S   N   N   L   D   E   P   P   V   F   D   A   P   A   D   V   A   I   S   D   A   D   R   E   L   D   S   L   V   P
2045 GAC TCG GCG AAC CAG CCG TAC GAC ATG CAC CGG GTC ATC GAG CAC GTG CTG GAC GAC GGG GAG TTC CTG GAG GTC CAG CCG CTG TAC GCG
    > D   S   A   N   Q   P   Y   D   M   H   R   V   I   E   H   V   L   D   D   G   E   F   L   E   V   Q   P   L   Y   A
2135 CAG AAC ATG GTG GTC GGC TTC GGT CGA ATC GAG GGA CGA CCG GTC GGC GTG GTG GCC AAC CAG CCG ATG CAC CTC GCC GGC ACG CTG GAC
    > Q   N   M   V   V   G   F   G   R   I   E   G   R   P   V   G   V   V   A   N   Q   P   M   H   L   A   G   T   L   D
2225 ATC GCC GCG TCG GAG AAG GCC GCC CGG TTC GTG CGC ACC TGC GAC GCG TTC AAC ATC CCC GTG CTG ACC TTC GTG GAC GTG CCC GGG TTC
    > I   A   A   S   E   K   A   A   R   F   V   R   T   C   D   A   F   N   I   P   V   L   T   F   V   D   V   P   G   F
2315 CTA CCC GGC ACC GGC CAG GAG TGG GAC GGC ATC ATC CGG CGC GGC GCG AAG CTC ATC TAC GCG TAC GCC GAG GCG ACC GTC CCG AAG GTC
    > L   P   G   T   G   Q   E   W   D   G   I   I   R   R   G   A   K   L   I   Y   A   Y   A   E   A   T   V   P   K   V
2405 ACC GTG ATC ACC CGC AAG GCG TAC GGC GGG GCG TAC GAC GTG ATG GGC TCC AAG CAC CTG GGC GCG GAT CTG AAC TTC GCC TGG CCG ACC
    > T   V   I   T   R   K   A   Y   G   G   A   Y   D   V   M   G   S   K   H   L   G   A   D   L   N   F   A   W   P   T
2495 GCG CAG ATC GCG GTG ATG GGC GCG CAG GGC GCG GTG AAC ATC CTG TAC CGG CAG GAG CTG GCC GCC GCC GAG GAC CCG GCC GCC GTG CGC
    > A   Q   I   A   V   M   G   A   Q   G   A   V   N   I   L   Y   R   Q   E   L   A   A   A   E   D   P   A   A   V   R
2585 GCC GAG AAG ATC GCC GAG TAC GAG GAC ACC CTG GCC AAC CCG TAC GTC GCC GCC GAG CGC GGG TAC GTC GAC TCG GTG ATC CCG CCG CAC
    > A   E   K   I   A   E   Y   E   D   T   L   A   N   P   Y   V   A   A   E   R   G   Y   V   D   S   V   I   P   P   H
2675 GAG ACG CGT ACC CAG ATC GTC CGG GCG TTG CGG GTG CTG CGC ACC AAG CGC GAG ACG CTC CCG GCG AAG AAG CAC GGC AAC ATC CCG CTC
    > E   T   R   T   Q   I   V   R   A   L   R   V   L   R   T   K   R   E   T   L   P   A   K   K   H   G   N   I   P   L
2765 TAG GCGCGGTGCAGGGAGGGGCCCCTGTCACGCGATCCGTGCAGCAGGGCCCCCTCCCGACGCCGGAGGAGCCGGCGGGCCCGGCAGCCGGGCGCCGG TCA GCA CGC CGG GTT
    > •                                                                                                   < •   C   A   P   N
2878 GGC GGC GAG GCA CAT CCG CCG GGC GGC CGT GCG GCC CAG TTC GAG CAG CTC CGC GTC GCT GGT CTC GCG GGG GCC GTC CGG CCC GTC GAC
    < A   A   L   C   M   R   R   A   A   T   R   G   L   E   L   L   E   A   D   S   T   E   R   P   G   D   P   G   D   V
2968 GCC CAA CCC GCG CTC GGG CAC GAT GAC GGT GAC CAG GTC GCC GAC CCG GAC GAT CAT CCG GGT TTC CGG CGG GTA CCC CAC GTC GAG GGG
    < G   L   G   R   E   P   V   I   V   T   V   L   D   G   V   R   V   I   M   R   T   E   P   P   Y   G   V   D   L   P
3058 CTT GCC CGT CGT GGG GTC CAC CGG GGA CAT CAC GGT GTG CCG CAA CAC GAC CGC CTC GTC GCC GGC GAA GTC GCG GGC GAT CGT CTG CCA
    < K   G   T   T   P   D   V   P   S   M   V   T   H   R   L   V   V   A   E   D   G   A   F   D   R   A   I   T   Q   W
3148 GGT GTG GGC CAC CGA GAT CGC GCC ACG GCC GTC GTC CAG GGG CCG AAC CGC CGT GTC GCT CCA GCG GGC GCA GGT GGT CGC CGC CCG GTC
    < T   H   A   V   S   I   A   G   R   G   D   D   L   P   R   V   A   T   D   S   W   R   A   C   T   T   A   A   R   D
3238 CAG GTC GGC GAG CAG CCG GCC GGC CGG GGC GGG GTC GAG GCG GTA GAC GTC CTG GGT GAG GAC GGG GAC GGC CAT CGA CCC GTC CTG GCC
    < L   D   A   L   L   R   G   A   P   A   P   D   L   R   Y   V   D   Q   T   L   V   P   V   A   M   S   G   D   Q   G
3328 CGA CGT GTC GTC CAG GAG CAG CGT CTG GGA TCG CGA GTA GCG AGA CAC CGG CGG CCC CGC CCC CGG CTC CTT GCC CAC GGC GCA CGA CTG
    < S   T   D   D   L   L   L   T   Q   S   R   S   Y   R   S   V   P   P   G   A   G   P   E   K   G   V   A   C   S   Q
3418 GAG CAG CGG GTC CAC CCG GAC CTG CTC CTG AAG CCC AGA GTC CCC CAG TCG TAC GTT GCT CGG CAC GCC CAG GTC GGC CGG GTC CAG CAG
    < L   L   P   D   V   R   V   Q   E   Q   L   G   S   D   G   L   R   V   N   S   P   V   G   L   D   A   P   D   L   L
```

FIGURE 12B

```
3508 GGC CTC CTG GCC GAT CTC GGT CCG GCC GGA CCG CTC CGG CTC GGT AGA CGC GCG CCA CCC GTC GAC CCA GGA CAT CGG CGG CGC GAG GTG
    < A   E   Q   G   I   E   T   R   G   S   R   E   P   E   T   S   A   R   W   G   D   V   W   S   M   P   P   A   L   H
3598 CCC GCC GGC CCG GCC GCC GAC CGC CAC GGC GAA GAC CGA GAG TAC GGC CAG CAC GGC CGC GGC CGC CGC CAT CGC CGT ACG CCG GCT GCG
    < G   G   A   R   G   G   V   A   V   A   F   V   S   L   V   A   L   V   A   A   A   A   A   M   A   T   R   R   S   R
3688 GCG GCG GGC CCG GGC GCG GAT GTC CGC CGG CTC GGG CCA ACG GAC GTC CCG CAG GTC CCG GTG CAT CCGTTCGGCGAACGTCAGGTCG TCA CGC
    < R   R   A   R   A   R   I   D   A   P   E   P   W   R   V   D   R   L   D   R   H   M                               <   •   A
3782 ATC GGC GGC CTC CTC CAG GTC AGA GAC GGC GAG CAG CCC GGC GAG CGC GGC ACG CCC CCG GGA GAG ACG GGC TTT CAC GGT GCC GAC CGG
    < D   A   A   E   E   L   D   S   V   A   L   L   G   A   L   A   A   R   G   R   S   L   R   A   K   V   T   G   V   P
3872 GGC GGC GGT CTC CCG TGC CAC CTC GGC CAC CGG CAT GCC GAG CAG GTA GTG CAG GGC GAT GGC GGT GCG CTG CGC CTC GGG CAG CCG GCG
    < A   A   T   E   R   A   V   E   A   V   P   M   G   L   L   Y   H   L   A   I   A   T   R   Q   A   E   P   L   R   R
3962 TAG CGC CGC CAC CAC CTC CAG CGT CGC GGT GCT CGG CGC GGG GAC GCT CTC CGG CGC ACC GTG CCG CAG GTA CGC CCG CGC CCG GCT ACG
    < L   A   A   V   V   E   L   T   A   T   S   P   A   P   V   S   E   P   A   G   H   R   L   Y   A   R   A   R   S   R
4052 CAT GCT GCG CCA CCG GCT CAC CGC GAT CCG GCT CGC CAC CAC GCG CAG CCA GCC CTC CGG ATC GTC GTA CCC GCG TAC GGT CGG CCA GCG
    < M   S   R   W   R   S   V   A   I   R   S   A   V   V   R   L   W   G   E   P   D   D   Y   G   R   V   T   P   W   R
4142 CTG CCA TGC GCG GAT GTA CGC CTC CTG CAC GGC GTC CTG CGC CTC GGC CAG GTT TCC GGT GAT CAT GTA CAC GAA ACC CAG CAA TCG TTG
    < Q   W   A   R   I   Y   A   E   Q   V   A   D   Q   A   E   A   L   N   G   T   I   M   Y   V   F   G   L   L   R   Q
4232 CCG GCT GCC CCG GTA GAA CTC GTC GAA CCC CTC GGC GTC CGG CAT CCGCCACCTCCCCGTGTCGCAGGGGACACGCCTGGCGGGTGGTCCCCGGTTGCCCGACCGG
    < R   S   G   R   Y   F   E   D   F   G   E   A   D   P   M
4338 CCGGCTTCTTCCCTCCCCGGGGGTCCCCGGCGGGTTCCTCCCGGGGTCTCCCGGCGGGCCCGTCACGTCACGGCCGGCGCGGCGGGCTCGTCACGTCACGGCCGGCGCGGCGGGCCTTCGG
4459 CAGCGAACAGCGACCGTCCGAGAATCGGGTGCCGGCCGGAGTGGTCGAGGGCGCGGGTGGGCGGTGG TCA GAC CGT GAG CCC GGC GTC GGT GAG GAT CGG GCC GGC
                                                                                                    <   •   V   T   L   G   A   D   T   L   I   P   G   A
4565 GAG CAG CAG GGC GCC GAC GGC GAG GCC GGC CAG GCA GAC GAC CAG GAA GAC ACC GAC CCA GAA CAG GGG CGG GAA CGG CGT CAA CCG GGC
    < L   L   L   A   G   V   A   L   G   A   L   C   V   V   L   F   V   G   V   W   F   L   P   P   F   P   T   L   R   A
4655 GAG CTG GTC GGC GTC GGA CTC CGG CAT CCG GCC ACG GCT GCG CAG CCG CTG CAA CTC GAT CAC CGG ACG CAC GCC GCC GAA CAG CAG GAA
    < L   Q   D   A   D   S   E   P   M   R   G   R   S   R   L   R   Q   L   E   I   V   P   R   V   G   G   F   L   L   F
4745 CCA GAC CGA GGT CCA GGC GAA CGC GGC CTG CAC CTG CGG CGG GGC GTA CCA GGA GAC GGC GAA GAC CAG ACC GCC GGT GGC GAG CAG CGA
    < W   V   S   T   W   A   F   A   A   Q   V   Q   P   P   A   Y   W   S   V   A   F   V   L   G   G   T   A   L   L   S
4835 CAG TGC CCC GTA GAC GTT GCG GAT CAT CGC CAG CAT GGC CAG CAG CAG CAC CAC CGT GAC CGA GAG CAG CAT GGT GAT CCG GTT CCC GGC
    < L   A   G   Y   V   N   R   I   M   A   L   M   A   L   L   L   V   V   T   V   S   L   L   M   T   I   R   N   G   A
4925 GAG CAG CCA CGC CCC GGC CAG CCC GAG CAG GGT CGG GGC GAC GTA CCC GGC GAA CAG GGT GAG GAT CAT GCC CAG CCC GGT GGG GCG GCC
    < L   L   W   A   G   A   L   G   L   L   T   P   A   V   Y   G   A   F   L   T   L   I   M   G   L   G   T   P   R   G
5015 GGC CGA CAG GGT GAG CCC GGA GGT GTC CGA GTG CAG CCG GAT GCC GCG CAG CTT CCG CCC GGT GAG CAG GGC GGC CAG CGC ATG ACC GCC
    < A   S   L   T   L   G   S   T   D   S   H   L   R   I   G   R   L   K   R   G   T   L   L   A   A   L   A   H   G   G
5105 CTC GTG GGC GAT GGT CAC CGC GTT ACG CGC GAC CCG CCA GGG CAC CCG GGT GGC GAC CAC CGC CAG CGC GAC GGC GGC GGT GGC CAG GAC
    < E   H   A   I   T   V   A   N   R   A   V   R   W   P   V   R   T   A   V   V   A   L   A   V   A   A   T   A   L   V
5195 CAG CAG CGG TGG CGG GTC GGG TTG CGC GCC GAC GAG TTC GTT CCA GAC GAC GCT CAG GCC GTC GAT CAG GTC CAC GGG GCC GCA GCC TAG
    < L   L   P   P   P   D   P   Q   A   G   V   L   E   N   W   V   V   S   L   G   D   I   L   D   V   P   G   C   G   L
```

FIGURE 12C

```
5285 CGG CCC CGG CCC GGT TCG CGC GCC GCG CGC CCG CCA CGG CCG CGG TGC CCG GCC CGG GCC CGG TCG ACC AGC GCC GGG GCG CAC GCCCGCCGC
    < P   G   P   G   T   R   A   G   R   A   R   W   P   R   P   A   R   G   P   G   P   R   G   A   G   P   R   V
5378 TGACCGGCACCCGG TCA GGT CGC GGG CAC CCC GGT CAG GTC GCC TGC GAC GAA GAA GGC CGC CGC TCT GGT GCC CAC CCG CAA CCG CCG CCG
                  < •   T   A   P   V   G   T   L   D   G   A   V   F   F   A   A   A   R   T   G   V   R   L   R   R   R
5470 AGG GCG GAC CTC ACC GAC CGG CGG CAC CTT GCG TCC ACG TAG GAC CAC GGC GAG CAC CCC GGT CGG CGG CAG CAC GGA AGC GAC CCT GGT
    < P   R   V   E   G   V   P   P   V   K   R   G   R   L   V   V   A   L   V   G   T   P   P   L   V   S   A   V   R   T
5560 CAG CAT CCC GGG CAG GCC CTC CCC GGC CCG CTC CCC CTG CCA GCT CGT CTG CTC CCC GTA CGG CAG GTC GGT CAC GAC CAG GTC GGG GGT
    < L   M   G   P   L   G   E   G   A   R   E   G   Q   W   S   T   Q   E   G   Y   P   L   D   T   V   V   L   D   P   T
5650 CAT GCC CGC GAC GGC CTC GGT GAG GGC CAC GCG GTC GAA CAC GTC GGC CCG CCG CAC CGC GTA CGG CAG CGG GCC GCC TGC CGC GTC CAG
    < M   G   A   V   A   E   T   L   A   V   R   D   F   V   D   A   R   R   V   A   Y   P   L   P   G   G   A   A   D   L
5740 ACG GGC GCG CAG CCG GTG GGC GGC GGC GGC CGC CTC CGC GTA GTG CGG CTT GTC GAA CGC CTC GGC GCG TTG CGC CAG CTC GCG GGC CCG
    < R   A   R   L   R   H   A   A   A   A   A   E   A   Y   H   P   K   D   F   A   E   A   R   Q   A   L   E   R   A   R
5830 CGT GTC GAG CCC GGC GCC GGT CAG CAG GCC GAG GTT GGC CCG AGC AAG GTC GAG GGC CGC CTC GTC GAC GTC GGA GGC GAG CAG CCC GGC
    < T   D   L   G   A   G   T   L   L   G   L   N   A   R   A   L   D   L   A   A   E   D   V   D   S   A   L   L   G   A
5920 AAG GCT CGG CCG GTG CAG CAG CGC GAG CAC CGT CAG CAG GTA GCC GCT GCC GCA GCA CGG GTC CCA GAC GGT GGC CGG GGC GGA CGT CGG
    < L   S   P   R   H   L   L   A   L   V   T   L   L   Y   G   S   G   C   C   P   D   W   V   T   A   P   A   S   T   P
6010 GCG CAA CTC CAG CGC GGT TTG CAG GAC CTC GGA GGC GAG CCG CAC CGG GAA CGC CGG GAA GCC CGG CGC CGA GCG CAA CAC GGC GCC ACT
    < R   L   E   L   A   T   Q   L   V   E   S   A   L   R   V   P   F   A   P   F   G   P   A   S   R   L   V   A   G   S
6100 GGC CAG GTC GCC GTA CGC ACC GCG TAC GGT TTC GTG CCG GTA AGT CAC ATG CCC TCC CCG GCG CAC CCT ACC AAT CCG GCA CCG CCG GGC
    < A   L   D   G   Y   A   G   R   V   T   E   H   R   Y   T   V
6190 CGG G TCA GGC AGG CCG GGA CTC GAT CCA GTG GAA GTC GGT GGG AGG CAG CGG CGT GAC GTC CTC CAG GGA CAG CCC CGC CTT GCC GCA CAG
          < •   A   P   R   S   E   I   W   H   F   D   T   P   P   L   P   T   V   D   E   L   S   L   G   A   K   G   C   L
6281 CCG TTC CAG GTC GCC TCG GGT CCG CTC CAG GCC CTG CCC GTT GAC CAG CAT CCC CAC GTC GGT CAG GTA CGC CAG CGC GTT GGC CGC CGG
    < R   E   L   D   G   R   T   R   E   L   G   Q   G   N   V   L   M   G   V   D   T   L   Y   A   L   A   N   A   A   P
6371 GCC GAC CAC GTC CGG CAG CAC GTG GTC GAT CAT GAC GAT CCG GCC GCC CGG GGC GAC CGC CTC GGC ACA GTG CCG GAG GAT TCC CGT CGC
    < G   V   V   D   P   L   V   H   D   I   M   V   I   R   G   G   P   A   V   A   E   A   C   H   R   L   I   G   T   A
6461 CCG GCC GTC GCC CCA ACC GTG GAT CAC ACT TTT GAG CAG GTA GAG GTC GGC GTC GGC GGG GAC CCT CTC GAA GAA GTC ACC CAC CTC GAT
    < R   G   D   G   W   G   H   I   V   S   K   L   L   Y   L   D   A   D   A   P   V   R   E   F   F   D   G   V   E   I
6551 CCG GCA CCG GTC GCC GAC CCC GGC GCG GCG CAG GTT CCC CGC CGC CTC CGC GCT GCC GCT GGC GCT GTC GTA GAG CAC GCC CCG CAC GCC
    < R   C   R   D   G   V   G   A   R   R   L   N   G   A   A   E   A   S   G   S   A   S   D   Y   L   V   G   R   V   G
6641 GGG GTT CGC GGC GAG CAC GGC GGC CAG CAG GGT GCC GTC TCC GCC GCC CAC GTC GAC CAC CGT CCG CAC GCC GGC CAG GTC GGT ACG CTC
    < P   N   A   A   L   V   A   A   L   L   T   G   D   G   G   G   V   D   V   V   T   R   V   G   A   L   D   T   R   E
6731 GGC AAC GGC CGC CGC GAC GCT GTG GGT CAC CTG GCT CAT CGC CGC GTT GTA CAG CTC GGA AAG GTC GGG TCG CCC GCC CAC GTA GCT GAA
    < A   V   A   A   A   V   S   H   T   V   Q   S   M   A   A   N   Y   L   E   S   L   D   P   R   G   G   V   Y   S   F
6821 GAA GTC GGT GCC GAA GAT GCC GTC GAA GGC CGG CTC GCC GGT GCG GAC GCT GTG CGC CAG GCC GTC CCA GGC CGT GGT CAT GGC CGG GTC
    < F   D   T   G   F   I   G   D   F   A   P   E   G   T   R   V   S   H   A   L   G   D   W   A   T   T   M   A   P   D
6911 GGT CAG CAT CCG GGC CAG CGG GCG CAG CGT GCC GGG TCG GTC CCC ACG CAG CAG CGC CCC CAT CGG GGC GAG CGC GAA CCG GCC GGG TGT
    < T   L   M   R   A   L   P   R   L   T   G   P   R   D   G   R   L   L   A   G   M   P   A   L   A   F   R   G   P   T
```

FIGURE 12D

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7001 GGT CTC GGT GAG CAC CCG CAG CGC GGC CAG GGC GCG CAG CAC CCG GAA CAT GGT GTC CGC TCG GGC GTC GTA CCG CAG CGC CAA CTC CTG
    < T   E   T   L   V   R   L   A   A   L   A   R   L   V   R   F   M   T   D   A   R   A   D   Y   R   L   A   L   E   Q
7091 CGG GGT GCG CTC GTC GTC GCC GAT CGC GTC GGG CAG CCC CAG CCG GAC GCA GTA GCC GAC CAG CCG GCT GGC CAT CCC GCC GAA CAC CAA
    < P   T   R   E   D   D   G   I   A   D   P   L   G   L   R   V   C   Y   G   V   L   R   S   A   M   G   G   F   V   L
7181 CCG CAT CAG CTC CGG CCA GGC GGC GTC CGC GCC GGT CTG CGC CCG GCG GGC GCT GGG CTC GTC GGT CGT CGT GGC CC GCTCGTCCGTGTCCGGGA
    < R   M   L   E   P   W   A   A   D   A   G   T   Q   A   R   R   A   S   P   E   D   T   T   T   A   R   E   D   T   D   P   V
7276 CGG TCA TCG GAC CGG CTC GGC GGC CGG CAG GCC CAG CCC GAT GCG CAC GGC CCG TTC GAC CGG CGA GTA GTC GCC GTC CGG GCG GTC CAG
    < T   M
        <   R   V   P   E   A   A   P   L   G   L   G   I   R   V   A   R   E   V   P   S   Y   D   G   D   P   R   D   L
7366 GTC CAG CTC GCC CAC CGG CTG CAG GCT CGG CTG GGC CAT GAA CCG GGG CCG CGT GCC GGT GTT GGC CAC CGG GGT GTG CAC CAG GAA CGG
    < D   L   E   G   V   P   Q   L   S   P   Q   A   M   F   R   P   R   T   G   T   N   A   V   P   T   H   V   L   F   P
7456 GTG GCA CAG GTA GAC GTC ACC GGC GCG TCC GGT GGC GGA GGC GAG CGG GCG GTC CCG GCC GAC GTC GCC CAC GTC GAG GTA GGT GCC CTC
    < H   C   L   Y   V   D   G   A   R   G   T   A   S   A   L   P   R   D   R   G   V   D   G   V   D   L   Y   T   G   E
7546 CGG GCC GTA CGG TTC GAG CAG CGG CGG CAC GTC CAG GTG GGA GCC GAC CCT GAC CAG CGT CGG CGC CTC CCG CTC GTC GGT GTC GGA GAA
    < P   G   Y   P   E   L   L   P   P   V   D   L   H   S   G   V   R   V   L   T   P   A   E   R   E   D   T   D   S   F
7636 GAG GAA CAG CAG CAG CAG GGC CCG CCC CCG CGA CCG GAG GTT GCA GCG GAA GAC CTC CGC GTA GTT GGG CGG GAC CAG GTC CAG CTC GCC
    < L   F   L   L   L   L   A   R   G   R   S   R   L   N   C   R   F   V   E   A   Y   N   P   P   V   L   D   L   E   G
7726 CTC CCA GTT CTG GGG GCC CAG CCG CTG CGC GTC GTC GGC CAG GAA ACT GGC GTC GAT GTG CCA GCC GTA GTC CTC GGT CTG CTC CGG GCG
    < E   W   N   Q   P   G   L   R   Q   A   D   D   A   L   F   S   A   D   I   H   W   G   Y   D   E   T   Q   E   P   R
7816 CTT GGG CAC CGG GAA CCG GAC CGG GAA GGT GCC GAT CCG GTC CAA CGG CTT CCA GCG CCC CAC CCC GAC GAG CTG GTC GAA GGC GGC GTG
    < K   P   V   P   F   R   V   P   F   T   G   I   R   D   L   P   K   W   R   G   V   G   V   L   Q   D   F   A   A   H
7906 CAG CCG GGG CGT GGT GGC GCT GCG CAC GAA GGG CTC GGC GTC CTG GAG GCC CAG CCG GAC CAC CTC GCG GGA CCA GGT GCT CCG GTC CTC
    < L   R   P   T   T   A   S   R   V   F   P   E   A   D   Q   L   G   L   R   V   V   E   R   S   W   T   S   R   D   E
7996 GGG GTC CAT GCC GAG TTG CCG CCA CAG CAG TTC GCG ACC CTG CTG CGC GAG CTC GGC CGG GAA CGC CGC CTC CAA CTT CAC GAA CCC GTC
    < P   D   M   G   L   Q   R   W   L   L   E   R   G   Q   Q   A   L   E   A   P   F   A   A   E   L   K   V   F   G   D
8086 GGA GAC GAA CCG CTC GAC CTG CTC GTC GCT GAG GAC CTG GGC GCT CAT CGC ACT CCT TCC CGC CGG TTC CCG CCG AGG CGG AGC GAG ACG
    < S   V   F   R   E   V   Q   E   D   S   L   V   Q   A   S   M
8176 GTC GCA CCC GCG CTG ACC GGA CCG GGC GAC GCG CCT CGT CAA GAT TCG CCA GGT TGA ATG GTA GAC AAG CCG CCA CCG TCA GGG ACT AAC
                                                                                                    <   •   P   S   V
8266 GTT TTC CTC AGC ATC GTC CGG GCC ACC GCG AGA GCG CCG CAC CCC CCG CTC CAC CAC CCG CAA CCA TCG GCT CTC CCC GGG TGC GGC GAT
    < N   E   E   A   D   D   P   G   G   R   S   R   R   V   G   R   E   V   V   R   L   W   R   S   E   G   P   A   A   I
8356 GCC GTC GAG CCG GGC GCG GGC CTC CTC CGG CAG CGG CCG GTC GGC CGC CGC CAG CGC CGC CCG GGC CTG GTC CAG CGT GCG GGG GCC GAC
    < G   D   L   R   A   R   A   E   E   P   L   P   R   D   A   A   A   L   A   A   R   A   Q   D   L   T   R   P   G   V
8446 GAC CGT GCT GGT CAC CCC CGG CGC GTC GTA GAC CCA GGC GTG CGC CAG GTC CGG CAG GGA CAG GCC CAG CTC GAC GGC CAC CTT CGC CAA
    < V   T   S   T   V   G   P   A   D   Y   V   W   A   H   A   L   D   P   L   S   L   G   L   E   V   A   V   K   A   L
8536 CCG GCC CAG GGT CCG CCA CAC CGG CTG CCA GTG CGG GCC CGA TGG GGC GTA CCA GGC GGT GAA CCG GGC GTC GCG GGG CGG CTC GCC GTC
    < R   G   L   T   R   W   V   P   Q   W   H   P   G   S   P   A   Y   W   A   T   F   R   A   D   R   P   P   E   G   D
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FIGURE 12E

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8626 GGC GAA CCG GTC GGA GAG CAG ACC CAT CGC CAG CGG GCT GTA GGT GAA CAG GCC GAG GCC GTA CTC CGC GCA CAG CGG CAG CAC GTC CCG
    < A   F   R   D   S   L   L   G   M   A   L   P   S   Y   T   F   L   G   L   G   Y   E   A   C   L   P   L   V   D   R
8716 CTC GAT CTC GCG TTC CAG CAG GTT GTA CGG CGA CTG CTC GGC CAC CAC CGG GGC GGC GCC CCG GGA CTG CGC CGT GCG CAG CAG GTC GAC
    < E   I   E   R   E   L   L   N   Y   P   S   Q   E   A   V   V   P   A   A   G   R   S   Q   A   T   R   L   L   D   V
8806 GAT CCG CCA GCT GGG CAC CGT GCC CAG CCG GGG CTG GTC GGC CAG CTC GTA TGC CGT GGG CAC GGT GGA GGT GCC CAC GTA GCG GAC CTT
    < I   R   W   S   P   V   T   G   L   R   P   Q   D   A   L   E   Y   A   T   P   V   T   S   T   G   V   Y   R   V   K
8896 GCC CGA GCG GAC CAG GTC GTC GAG GGC GGA CAC CGT CTC CTC CAC CGG AGT GTC CGG GTC GTG ACG GTG CAG GTA GAG CAG GTC GAT GTG
    < G   S   R   V   L   D   D   L   A   S   V   T   E   E   V   P   T   D   P   D   H   R   H   L   Y   L   L   D   I   H
8986 GTC GGT ACC CAG CCG GCG CAA CGA CCG CTC GCA CTC CCG CTT CAG GGC GTA CGC CGA GGT GCC CCG GTC GTT CGG TCC CGG GCC GAC CGG
    < D   T   G   L   R   R   L   S   R   E   C   E   R   K   L   A   Y   A   S   T   G   R   D   N   P   G   P   G   V   P
9076 ATT GAA GAT CTT GGT GGC CAG CAG GAC GTC GTC CCG GCA GCT CCG CAC GGC CGC GCC GAC GAT CTC CTC GCT GCG GCC GTC CTG GTA GAC
    < N   F   I   K   T   A   L   L   V   D   D   R   C   S   R   V   A   A   G   V   I   E   E   S   R   G   D   Q   Y   V
9166 GTT GGC CGT GTC GAC GAG GTT GAC TCC CGC TTC GAC GGC CGT GGC GAC GAT CCT GGC GGC CTC CTC CGG CCC GGT CGG GCC GCC GAA GTT
    < N   A   T   D   V   L   N   V   G   A   E   V   A   T   A   V   I   R   A   A   E   E   P   G   T   P   G   G   F   N
9256 GAA CGC CCC CAG GGA CAC CTT GGA CAC CCG CAG TCC ACA CCG GCC CAA CTG TCG GTA CTC CAC GCTGCCCTCCCCTGCGGTGGTGGTCGCCGGCCACCC
    < F   A   G   L   S   V   K   S   V   R   L   G   C   R   G   L   Q   R   Y   E   V
9355 CGTCGTGCGGCCGGTGCTCCCCGGAGCCGGGGAGTGGCCGATCTCGATGGGGGAGCCTAGTACCGCGCGGGTGCCTCGGCCGTGGTACTAGCAGAACTGCTAG AGC ATC CGT CGA
9470 GCC GCC GGG CGG CCG GGC GGC AGC CGG TAC GGT GTG CCT GAA CCC ACC ACG GGC CGG CGC CGG ACG ACC GGT CGA CGA GCG ATC GAG CTG
9560 ATC GGC GGG GAG CGG ATG AGC GAC AAG TAC GGC CGC AGT GCG CTG TGG GAA CGG TAC AAC AGC ACA CAG GTG ACC GAG GAG GCG GCG GAC
                        > M   S   D   K   Y   G   R   S   A   L   W   E   R   Y   N   S   T   Q   V   T   E   E   A   A   D
9650 GAC CTC ACC TCC TTC AAG TCG AGC GAC GTC AAC TAC AAG CTC GCC CTC TGG GAT CCC CGG GTC AGC GGG GTC CGC TAC CTG AAG ACG CTC
    > D   L   T   S   F   K   S   S   D   V   N   Y   K   L   A   L   W   D   P   R   V   S   G   V   R   Y   L   K   T   L
9740 ATC TTC AAC CTG GCC GAG AAC CTG GGC GAG GCG AAC CGG GCC CGG TTG CGC CGG ATC GCC AAC CGG GAC GTC GGC GAC CCC ATC TCC GTC
    > I   F   N   L   A   E   N   L   G   E   A   N   R   A   R   L   R   R   I   A   N   R   D   V   G   D   P   I   S   V
9830 GTC TGG GAC GGC GAC CGG ATC TGC ATG GAC TAT CTC CAG GCG GTG CTG GAG CTG GAG TTC TTC TCC CGC CAC GTG CCA CTG GAC GGC GCG
    > V   W   D   G   D   R   I   C   M   D   Y   L   Q   A   V   L   E   L   E   F   F   S   R   H   V   P   L   D   G   A
9920 ACG GTG CTG GAG ATC GGC GCG GGC TAC GGC CGC ACC TGT CAC GCC GTG CTC TCC AAC CAC GAC GTC GCC GCG TAC CAC GTG GTC GAC CTG
    > T   V   L   E   I   G   A   G   Y   G   R   T   C   H   A   V   L   S   N   H   D   V   A   A   Y   H   V   V   D   L
10010 CCG AAC TCC CTC GCT CTG GCC CGC CGC TAC CTG GGC ACG GTG CTC ACC GCC GAG CAG TTG GCG AGG GTC CAC TTC CAC GGC GTC GGC GAG
    > P   N   S   L   A   L   A   R   R   Y   L   G   T   V   L   T   A   E   Q   L   A   R   V   H   F   H   G   V   G   E
10100 GTG GAC GGG CCG CTG AGC GAG CTG CGC TAC GAC CTC GTG ATC AAC ATC GAC TCG TTC GCG GAG ATG ACG GCG GAG ACG GTG CGC GCG TAC
    > V   D   G   P   L   S   E   L   R   Y   D   L   V   I   N   I   D   S   F   A   E   M   T   A   E   T   V   R   A   Y
10190 CTC GCC TTC GTC GCC ACC AGG GCC CGC CAC CTG TAC GTC AAC AAC CCC GTC GGG AAG TAC CTC GAC AAG AGC CTG GAC GGG CAC TTC CAG
    > L   A   F   V   A   T   R   A   R   H   L   Y   V   N   N   P   V   G   K   Y   L   D   K   S   L   D   G   H   F   Q
10280 GGC GAG GCC GTG GTC AAC CTT GCG CTG AGC ACC GGC CTG CTG CGC GAC GTC ATC GAC ATC CAC GAC AAC CAG GCC GTG CGG CGG CAG TCC
    > G   E   A   V   V   N   L   A   L   S   T   G   L   L   R   D   V   I   D   I   H   D   N   Q   A   V   R   R   Q   S
10370 CGG GCG TTC CTC GAC GCG TAC CGG CCG GGG CCG GGC TGG GCC TGC GTG GCG GAG AGC CGG ACG ATC CCG TGG AGC TAC TAC TGG CAG GCG
    > R   A   F   L   D   A   Y   R   P   G   P   G   W   A   C   V   A   E   S   R   T   I   P   W   S   Y   Y   W   Q   A
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FIGURE 12F

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10460 CTC TAC CGG GCC GGC GAG GCG GCC CCG GCA CCC GGG CGG GAT TGA GGTGACCGGCCGAGCGGGCGAGCCCGCCGACCGGCCCGTCGTCGCCGTCCTCGGCGCCTCC
     > L   Y   R   A   G   E   A   A   P   A   P   G   R   D   •
10566 GGCCTGGTCGGCACCGCT GTG CTG GCC GCG CTC GCC GAC CGG GCG GTC ACC GTC CGG GCC GTC GCC CGC CGG GCT GCC GTG CTG CCC GCC GCG
                       > V   L   A   A   L   A   D   R   A   V   T   V   R   A   V   A   R   R   A   A   V   L   P   A   A
10659 CCG GGC CGC GCG GCG TTT GAG GTG GTA CGG GCC GAC CTG ACC GAC CGG GGA GCC CTG GCG GCG GCG GTA CGC GAC GCG ACG GCC GTG GTC
     > P   G   R   A   A   F   E   V   V   R   A   D   L   T   D   R   G   A   L   A   A   A   V   R   D   A   T   A   V   V
10749 AAC CTC ACC CTG GAC AGT TCC GGC TGG CGG GGC GCC GAC GAC GAC CGC AGC GCG CGG GTC AAC GTC GAG CTG ACC CGG GAA CTC GTC GGG
     > N   L   T   L   D   S   S   G   W   R   G   A   D   D   D   R   S   A   R   V   N   V   E   L   T   R   E   L   V   G
10839 ATG CTC CGC CCC GGG CCG GGC GGC ACG CCC ACC ACA CTG GTC TTC GCC GGC TCC GCC TCC CAG GTG GGC CGG CCG CCC CGG ATC CCG ATC
     > M   L   R   P   G   P   G   G   T   P   T   T   L   V   F   A   G   S   A   S   Q   V   G   R   P   P   R   I   P   I
10929 GAC GGC ACC GAG CCG GAC CAC CCC GCC ACC CCG TAC GAC CGG CAG AAG CAG GCC GCG GAG TCG CTG GTC GTG GCG GCC ACC GGG GCC GGC
     > D   G   T   E   P   D   H   P   A   T   P   Y   D   R   Q   K   Q   A   A   E   S   L   V   V   A   A   T   G   A   G
11019 GTC GTG AAC GGG GTG TCG CTG CGA CTG CCC ACC GTG TTC GGC CCG GTG CCG CCG GGC GCC GGG CCC GAC CGG GGC GTG GTG TCC ACG ATG
     > V   V   N   G   V   S   L   R   L   P   T   V   F   G   P   V   P   P   G   A   G   P   D   R   G   V   V   S   T   M
11109 ATC CGC CGG GCG CTG TCC GGA GCG CCA CTG ACC ATG TGG CAC GAC GGC CGG GTG CAA CGG CAA CTG CTG TAC GTG GCC GAC GCC GCC GCC
     > I   R   R   A   L   S   G   A   P   L   T   M   W   H   D   G   R   V   Q   R   Q   L   L   Y   V   A   D   A   A   A
11199 GCC TTC GTG GCG GCG CTG GAC CAC CCC GGG GCG CTG ACC GGC CGG CAC TGG CCG CTC GGC GAC GGC CGG GGT GAA CGG CTC GGG GAC CTG
     > A   F   V   A   A   L   D   H   P   G   A   L   T   G   R   H   W   P   L   G   D   G   R   G   E   R   L   G   D   L
11289 TTC CGC GCC ATC GCC GCC CTG GTG GCC GAG CGG ACC GGT CGG CCA CCG GTG CCG GTG CTG GCC GTG CCC CCG CCC GAC GAG GCC CGG GTC
     > F   R   A   I   A   A   L   V   A   E   R   T   G   R   P   P   V   P   V   L   A   V   P   P   P   D   E   A   R   V
11379 AGC GAC TTC CAC GAC ATG GTC GTT GAC GCC TCG GCC TTC CAG GCG GTC ACC GGG TGG GCG CCC CGG GTG CCG TTG CGC CTC GCG CTG GAC
     > S   D   F   H   D   M   V   V   D   A   S   A   F   Q   A   V   T   G   W   A   P   R   V   P   L   R   L   A   L   D
11469 CGC ACC GTC GCG GCG CTC GCC CGC GAC GAC AGC GGC CCC GAG GCC CCG GGC GGC GTC GGC CCG ACG CGG GCG GAT CAG GCC CGG
     > R   T   V   A   A   L   A   R   D   D   S   G   P   E   A   P   G   G   V   G   P   T   R   A   D   Q   A   R
11553 AAG CCG GAC TCG ATC TCC AGG CAG GTC CGG TAG TCGGGCAGCAACCCACGGGCGAGCGCCTGGTCGAAGGTGATCGCGGTGCGGTCCCGCTCCGACAGGATCGGTTCGAC
     > K   P   D   S   I   S   R   Q   V   R   •
11663 GTCCTCGGGGATGGGCAGGCCCAGCCCGGGGTCGAGCGCGTCGAGCGCCAGTTCGTTCTCGAAGACGTACTCCTGGGACAGGACGTACGACATGACGGTGTCGTCGGCCAGGGCGACGAAC
11784 ATGTGCGCGACCCCGACCGGCAGGTAGACCGCCTGGAACTCCTCGCTGTCGAGCACCACGCTGTCCCACTTGCCGAACGTCGGTGAGCCCACCCGCACGTCGAGGACCAGGTCGAGCACCC
11905 GGCCGTGCGGGCAGGAGACGAACTTCGCGGTGCCGGGCGGGGTACGGGTGAAGTGCAGCCCCCGCAGCGTCCCCCGGCGGGAGACGCTGTAGCTGGTCTGCCGCACGGGGAACAGCGGGTA
12026 CCCGACCGTGTCCCGGAACAACGAGTCGAGATACGGCGAGAGGAACACCCCCCGGTAGTCCGGGTAGACGGTGGGCGCGAAGGCGTACGCGCCTTCGACGGTCAGCGGGCGGGCGGACACC
12147 GGCGGG
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FIGURE 12G